E05467 DNA sequence 236077 S.cerevisia M64956 Yeast urea AL031347 Human DNA AC00584 Homo sapi U17165 Cricetulus

X03833 Human gene AL078622 Homo sapi 05467 DNA sequenc

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Unclassified.

1 (bases 1 to 20)

Kornman,K.S. and Duff,G.W.

Notecting genetic predisposition to periodontal disease Patent: US 5686246-A 2 11-NOV-1997;

Location/Qualifiers
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Sequence 2 from patent US 5686246.
173226
                        E03467
SCYBR208C
SCYBR208C
AC005884
AC005884
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HS106502
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AC007253
AC007288
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AC007288
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H8447D17
H8X1STA
HWXIST
AC005291
HSXIST2
AC005818
MUSRP105
HSDU93K22
  HSIL1AG
HSDJ925J7
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AE000848
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AUTHORS
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                                                                                      September 18, 1999, 15:49:42; Search time 436.05 Seconds (without alignments) 145.865 Million cell updates/sec
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                GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                                                    679419 segs, 1590154680 residues
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                                                                 nucleic search, using sw model
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em_htg:*
em_hum1:*
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23-DEC-1997

PAT

DB 5; Length 20; 0.22;

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AF098256 Pseudomon 267750 S.cerevisia x04287 Yeast Cell x03246 Yeast Cocy 274213 S.cerevisia b87014 Human (lamb x02505 H.sapiens g AL022476 Human DNA AC000027 Homo sapi AC000027 Homo sapi AC007558 Homo sapi AC007558 Homo sapi AC007253 Homo sapi AC005203 Arabidops AL021367 Human DNA X56199 Human X157, M97168 Homo sapien AC005291 Homo sapien AC005291 Homo sapien AC005291 Homo sapien AC005301 Homo sapien AC005301 Homo sapi AC005301 Homo sapi AC005301 Homo sapi AC005302 Mus muscu AE0000848 Methanoba Y10532 S.mitis pbp AC007140 Homo sapi

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Eukaryota: Mattazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eukharyota; Metazoa; Catarrhini; Hominidae; Homo.

Eukharyota; Metaroa; Catarrhini; Hominidae; Homo.

Eutharyota: Different of the sufficient of the sequence Campus, Hinxton, Submitted (11-JUN-1999) Wellcome Trust Genome Campus, Hinxton, Submitted (11-JUN-1999) Wellcome Trust Genome Campus, Hinxton, Submitted (11-JUN-1999) Wellcome Trequests: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk numquery@sanger.ac.uk Clone is unfinished and does not necessarily IMPORTANT: This sequence is unfinished on the sequence is in progress and the release of this data is based on the sequence may be sequence may change as work continues. The sequence may be sequence with foreign sequence from E.coli, yeast, vector, contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished: dJ92237 Contig_ID: Length: 13921 bp Unfinished: dJ92237 Contig_ID: acc=AL078622 Length: 18921 bp Unfinished: dJ92237 Contig_ID: acc=AL078622 Length: 18921 bp Unfinished: dJ92237 Contig_ID:
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HOMO Sapiens chromosome 22 clone DJ925J7, WORKING DRAFT SEQUENCE,
in unordered pieces.
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95.0%; Pred. No. 2.6;
Live 0; Mismatches 1;
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1 2489 c 2226 g 3547 t
                                                                                                                                                                         repetitive sequence"
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8912. 9137

/note="5 x 46 bp repeat"

9770. 9806

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7815 .7939
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HTG; HTGS_PHASE1.
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7940. .10289
/number=6
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6262. .6432
                                       3215. .4102
/number=3
4103. .4325
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7695. .774
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3166. .321
/number=3
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LTAISJATION="MAKVPDMFEDLENCYSENEEDSSSIDHLSLNQKSFYHVSYGPLH

EGCMDQSVSLSISETSKIFKESMVVVATNGKVLKKRELSLSOSITDDDLEALAN

DSEEDIIKPRSSPFSFLSNVKYNFMAINIKYEFILNDALNQSIIRANDOYLTAAALHNL

DEAVKFDMAKTKSKDDAKITVILRISKTQLYVTAQDEDQPYLLKENPEIPKTITGSE

TNLLFFRETHGTKNYFTSVAHPNLFIATKQDCYWVCLAGGPPSITDFQLENQA"

2208. .3165
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Carthini; Hominidae; Homo.
1 (bases 1 to 11970)
Furutani,Y., Notake,M., Fukui,T., Ohue,M., Nomura,H., Yamada,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erratum:[[published erratum appears in Nucleic Acids Res 1986 Jun 25:14(12):5124]]
Data kindly reviewed (10-NOV-1986) by Y. Furutani.
Location/Qualifiers
1. 01700
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/db_xref="taxon:9606"
eature 254...393
_roce="Alu repetitive sequence"
_region 1375...1382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete nucleotide sequence of the gene for human interleukin 1
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6262. 6432,7815. 7939,10290. 11643)
1489. 2152
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7815. .7939,10290. .10490)
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                                                                                                                                                                                                                                                        X03833.1 GI:33785
Alu repetitive sequence; interleukin 1 alpha; inverted repeat;
repetitive sequence.
                  Gaps
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                      Indels
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/note="inverted repeat A'"
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/note="direct repeat 1"
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                      Mismatches
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1375. .1382
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1438. .11643
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PP 24-SEP-1993
PF 05-MAR-1992 JP 1992084531
PF NSHRR-1992 JP 1992084531
PF NSHR-1992 JP 1992084531
PF NSHR-1992 JP 1992084531
PF OCCLORAL SCGABE YUKIHIRO, AISUI SHIGENORI PC C12R1:865),
CC CLINSY88.CI2R1:865);
CC Strandedness: Double;
CC Strandedness: Double;
CC Apportation No;
CC Apportation No;
CC Anti-sense: Act ain-ATCC44769;
FH Key Location/Qualifiers
FT 5'UTR 1: 684
FT CDS 685. 6192
FT 7'UTR 6193. 6265.
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Saccharomyces cerevisiae.
Eukaryota; Fungli, Ascomycota: Hemiascomycetes; Saccharomycetales;
Saccharomycetacae; Saccharomyces.

1 (bases 1 to 6265)
Nishiya,Y., Sogabe,Y. and Aisui,S.
DNA HAVING GENETIC INFORMATION OF UREAAMIDOLYASE AND ITS USE
PATENT: JP 1993244959-A 1 24-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E05467 6265 bp DNA PAT 29-SEP-1997
DNA sequence encoding Saccharomyces cerevisiae urea amidolyase.
E05467
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00363 acc=AL078622 Length: 27242 bp Unfinished: dJ925J7
Contig_ID: 01058 acc=AL078622 Length: 56385 bp Unfinished:
4.00TE: This is a 'working draft' sequence
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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685. .6192

/product='urea amidolyase'

R 6193. .6265.
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/db_xref="taxon:4932"
1156 c 1361 g 1875 t
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27752 c 27696 g 30553 t
                                                                                                                                                                                                                                                                                                                                           84.0%; Score 16.8; D
90.0%; Pred. No. 24;
tive 0; Mismatches
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Best Local Similarity 94.4%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                     /organism="Homo sariens"
/db_xref="taxon:9605"
                                                                                                                                        Location/Qualifiers
1. .118605
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JP 1993244959-A/1.
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ALEST Submission

ALE Submitted (30-AUG-1994) Data collected by MIPS on behalf of the European yeast chromosome II sequencing project. MIPS at the European yeast chromosome II sequencing project. MIPS at the European yeast chromosome II sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152

Estable Mann, M. Aljhowic, S. Andre, B. Baclet, M.C., Barthe, ... Baur, A. Becam, A.M., Bissereau, F. Christiansen, C., Contreras, R., Crouzet, M., Bussereau, F., Christiansen, C., Contreras, R., Dondey, H., Duscethus, C., Dubois, E., Dujon, B., El Bakkoury, M., Entian, K.D., Feuermann, M., Fiers, W., Fobo, G.M., Fritz, C., Gassenhuber, H., Glansdorff, N., Goffeau, A., Givell, L.A., de Haan, M., Heln, C., Jacquet, M., Jauniaux, J.C., Jonniaux, J.L., Kallesoe, T., Kiesau, P., Kirchath, L., Koetter, P., Korol, S., Liebl, S., Logghe, M., Kiesau, P., Kirchath, L., Koetter, P., Korol, S., Liebl, S., Logghe, M., Nassenguy, F., Miosga, T., Molemans, F., Mueller, S., Mannhaupt, G., Messenguy, F., Miosga, T., Molemans, F., Mueller, S., Pohnzilose, C., Stala, J., Slonians, P. P., Snits, P. H.M., Souciet, J.L., Steensam, H. Y., Stucka, R., Urrestarazu, A., van der Aart, O.J., van Dyck, L., Vassarotti, A., Valle, M., Kolle, K.H., Zagulski, M., Zimmermann, F. K., Mewes, H.W. and Kleine, K. Complete DNA sequence of yeast chromosome II
                                                                                                                                                                                                                                                                                                                 baker's yeast.
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                    S.cerevisiae chromosome II reading frame ORF YBRz08c.
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Feldmann, H., Mannhaupt, G., Schwarzlose, C. and Vetter, I.
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Bussereau,F., Demolis,N., Jacquet,M. and Mallet,L.
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/db_xref="taxon:4932"
/chromosome="II"
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/db_xref="PID:9536588"
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/gene="DUR1,2"
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/gene="DUR1,2"
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4 (bases 1 to 6042)
937 TIGCATAIGAGCCTICCA 954
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FDQYEEYPYEDEDLEKHTEDCDNGYYKNIEKSYFDHQEXLARTNANDSITAROPGQ
EGRAEEFERKIIQNANSELKESYTYKPDEEDFPEGABIYYSEYSGRFWKSIASVGDV
IEGAGGGLLIIEAMKREMIISARKSGKIKIICHGNMCDSGDIYAVIETLA"
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FVPLSYESSRSLKESQDVAIKSLDGTKLRRLDSVSILPSFETPILAQMEKVNELSPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGVTCGPHGSPDFFKPESIEEFFSEKWKVHYNSNRFGVRLIGPKPKWARSNGGEGGMH
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                                                                                                        SSAGSASVVARGIVPIALGIDIAGSGRVPAALNNLIGLKPIKGVFSCQGVVPACKSLD
                                                                                                                                         CVSIFALNESDAERCFRIMCQPDPDNDEYSRPYVSNPLKKFSSNVTIAIPKNIPWYGE
                                           VAPVDNAWISLISKENLLHQFQILKSRENKETLPLYGVPIAVKDNIDVRGLPTTAACP
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Saccharomycetaceae; Saccharomyces.
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Genbauffe, F. S. and Cooper, T. G.
The urea amidolyase (DUR1, 2) gene of Saccharomyces cerevisiae
DNA Seq. 2 (1), 19-32 (1991)
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Yeast urea amidolyase (DUR1.2) gene, complete cds.
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    6141
/organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"

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Pred. No. 35;
0; Mismatches
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/gene="DUR1.2"
/db_xref="SGD:S0000412"
241..5748
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/gene="DUR1.2"
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94.4%;
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Matches 17; Conservative
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HGTTAACTYLDMNKTIDAAKOTNAQAIIPGYGFLSENADFSDACTSAGITFVGPSGDI
GKGLGKHSARQIAQKAGVPPGSGLILTSVEREKKVAAELELPPWWYRSTAGGGGIGL
OKUDSEEDIEHIFFSTAGIAGVEFUPGDAGVELKRFTENARHVEVQLAGDGFGKAIALGE
RDCSLORRNQKVIEETPAPNLPEKTRLALRKAAESLGSLLNYKCAGTVEFIYDEKKDE
FYFLEVNTRALQVEHPTTENATGLDLVEWMIRIAANDAPDFSDFSVKVEWVBCSKENE
ENPLKNRFRESPGLLVDVKFPDWARVDTWVKGTNISPESTVEVKUVSVERIYA
KLNQALEETKVYGCITNIDYLKSIITSDFFAKAKVSTNILNSYQYEPTAIEITLPGAH
TVIATIGGTALGTLGDGEIPQHKPVEVKRGSTLSIGNDXIS
TVIATIGGTALGTLGDGEIPQHKPVEVKRGSTLSIGNDXIGTGGTIDVPKYL
GSYSTFTLGGTALGTLGDQEIPQHKPEVKRGSTLSIGLTGGTAGINGGTIDVPKYL
GSYSTFTLGGNVGGTNGRVLKLGDVLFLPSNEENKSVECLPONIPQSLIPQISETKERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKNPVLFSNAVENLSRTGANTIEIDFEPLLELARCLYEGTWYAERYQAIQSFLDSKPP
KESLDPTVISIIEGAKKYSAVDCFSFEYKRQGILQKVRRLLESVDVLCVPTCPLNPTM
QQVADEPVLVNSRQGTWTNFVNLADLAALAVPAGFRDDGLPNGITLIGKKFTDYALLE
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VOLEKVNATTLGTTKTSKAYOLFALLSKNGPVLRFGLRRVODSNSQIELEVYSVPKEL
FGAFI SMYPEPLGISSEWIKSFICEESGYKAKGTVDITKYGGFRAFEMLKK
KESOKKKLFDTVLIANRGEIAVRIIKTLKKLGIRSVAVYSDPDKYSGHVTDADVSVPL
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PSNTHDYVYSLGAINFTGDEPVIITCDGPSLGGFVCQAVVPEAELWKVGQVKPGDSIQ
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YNPSRTYTERGAVGIGGMYMCIYAANSPGGYQLVGRTIPIWDKLCLAASSEVPWLMNP
FDQVEFYPVSEEDLDKMTEDCDNGVYKVNIEKSVFDHQEYLRWINANKDSITAFQEGQ
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Human DNA sequence from clone 596H12 on chromosome 6p22.2-22.3.
Contains ESTs, STSs and GSSs, genomic marker D6S461 and TC, CA and
TA repeat polymorphisms, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                 SSAGSASVVARGIVPIALGTDTAGSGRVPAALNNLIGLKPTKGVFSCQGVVPACKSLD
CVSIFALNLSDAERCFRIMCQPDPDNDEYSRPYVSNPKKNFSSNVTIAIPKNIFWYGE
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IEAGGGLLIIEAMKAEMIISAPKSGKIIKICHGNGDMVDSGDIVAVIETLA"
                                                                                                                                                /protein_id="AAC41643.1"
/db_xref="PiD:q173122"
/db_xref="G1:173122"
/db_xref="G1:173122"
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                                                                                                                                                                                                                                                                                                                                                 SFAYEPSKDSKVVELLRNAGAIIVGKTNLDQFATGLVGTRSPYGKTPCAFSKEHVSGG
                                                                                                                                                                                                                                                                                                         VAPVDNAWISLISKENLLHQFQILKSRENKETLPLYGVPIAVKDNIDVRGLRTTAACF
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Submitted (23-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA. UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175555)
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HTG; CA repeat polymorphism; D6S461; TA repeat polymorphism;
repeat polymorphism.
/codon_start=1
/function="hydrolysis of urea to ammonia and CO2"
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Pred. No. 35;
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requests: clonerequest@sanger.ac.uk
On Jan 16, 1999 this sequence version replaced gi:3927943.
On Jan 16, 1999 this sequence version replaced gi:3927943.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence is the entire insert of clone 596H12. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       710. .840 https://dolem.com/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/predictions/pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 5964H2 is from the library RPC14 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="HERV16 repeat: matches 1571. .1944 of consensus"
6293. .6503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="HERVL repeat: matches 4443. .4661 of consensus" 087. .7374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .6146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.230. .2825
hote="HERV16 repeat: matches 328. .940 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           913. .8039
note-"LTR16A repeat: matches 317. .442 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2/80. .1302/
note="LIME repeat: matches 5533. .5788 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1540. 1928
/note="LTRich repeat: matches 18. .440 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              762. .8831
note="MSTA repeat: matches 361. .426 of consensus"
832. .9142
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1143. .9475
1061-"MSTA repeat: matches 1. .361 of consensus"
1222. .9706
100te-"match: GSS AQ219540"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14101. .14503 // hote="L2 repeat: matches 972. .1381 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L1PA2 repeat: matches 5669.
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/note="AluSg repeat: matches 1.
complement(11134. .11527)
/note="match: GSS AQ086021"
complement(11525. .11848)
/note="match: GSS AQ062320"
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13027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"/db_xref="taxon:9606"
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'note="AluJb repeat:
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710. .840
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/map="p22.2-22.3"
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/note="MIR repe
12780. .13027
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complement(6792. .6820)
/rpt_family="(CA)n"
complement(6888. .6898)
/rpt_family="Charliel"
6899. .7192
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complement(1997, .2070)
/rpt_family="L2"
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312. .6407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(3529, 3821)
/rpt_family="Aluy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5510. .5833)
/rpt_family="L1M4c"
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671. .6776
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524. .6663
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/rpt_family="LIME3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136. .253
/rpt_family="MIR"
1699. .1783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'rpt_family="MIR" 197. .5497
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                               ton 401/4. .40709

/note="MER41C repeat: matches 9. .554 of consensus"
/note="LIFR16B repeat: matches 137. .304 of consensus"
/note="MER50 repeat: matches 137. .304 of consensus"
/note="MER50 repeat: matches 1. .722 of consensus"
/note="MER5B repeat: matches 69. .178 of consensus"
/note="MER5B repeat: matches 59. .178 of consensus"
/note="LIM01 repeat: matches 5555. .6325 of consensus"
/note="MER4194 repeat: matches 1. .167 of consensus"
/note="FRAM repeat: matches 1. .167 of consensus"
/note="LIM04 repeat: matches 1. .167 of consensus"
/note="LIM04 repeat: matches 1. .371 of consensus"
/note="THE1C repeat: matches 1. .371 of consensus"
/note="THE1C repeat: matches 1. .371 of consensus"
/note="THE1C repeat: matches 1. .370 of consensus"
/note="THE1C repeat: matches 1. .350 of consensus"
/note="THE1C repeat: matches 1. .371 of consensus"
/note="THE1C repeat: matches 1. .350 of consensus"
/note="THE1C repeat: matches 1. .350 of consensus"
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Homo sapiens chromosome 17, clone hRPR.264_B_14

Unpublished
(Chases I to 120187)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barkr, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gardyna, S., Geraigery, K., Grant, G., Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J.,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 120187)
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/note="THELC repeat: matches 1. .371 of consensus"
             /note="WERSB repeat: matches 62. .120 of consensus"
40174. .40709
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17, clone hRPK.264_B_14, complete
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Best Local Similarity 94.4
Matches 17; Conservative
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AC005884/c
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TITLE
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SOURCE
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Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thoman, N., Silhwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vassiliev, H., Vo. A., Magner, A., Wheeler, J., Wu, Y., Wyman, D., Yew, W., Tano, J. and Zody, M.

Interf. Submission

N. Edward, J. Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 120 Charles Street, Cambridge, MA 02141, USA

Research, Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Brown, A., Castle, A., Carly, J., Colangelo, M., Collins, S., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gardyna, S., Garajary, M., Grant, G., Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vassilkev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ver, S., Land, S., Land, C., Land, C.,
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Submitted (10-NOV-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 10, 1998 this sequence version replaced 91:3850604.
All repeats were identified using RepeatMasker: Smit, A.F.A. 6
Green, P. (1996-1997)
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Cricetulus migratorius
Cricetulus migratorius
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
U thases 1 to 766)
Whitters,M.J. and Collins,M.
Hamster cDNA homologs to the mouse immunoglobulin kappa constant and Igk-V 45.1 genes
Immunogenetics 42 (3), 227-228 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission

Loudide (15-004-1994) Mary Collins, Genetics Institute, 87

Cambridge Park Dr., Cambridge, MA 02140, USA

Location/Qualifiers

1. 973

/ Organism="Cricetulus migratorius"

/ db_xref="taxon:10032"

/ dev_stage="rearranged"

50. 769

/ con_start=1

/ product="immunoglobulin kappa light chain"

/ db_xref="Gi:841148"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CMU17165 973 bp mRNA ROD 04-DEC-1995 Cricetulus migratorius Ig kappa light chain mRNA, complete cds. U17165 9841147 U17165.1 GI:841147
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Best Local Similarity 94.4%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches
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30257. .30440
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Collins, M.
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VNNFYPKDINVKWKVDGSEKRDGVLQSVTDQDSKDSTYSLSSTLSATRADYEBRNLYT
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Volke,S.T., Barak,J.D., Henderson,D.M. and Gilbertson,R.L.
Bacterial blight of leek: A new disease in California caused by Pseudomonas syringae
Plant Dis. (1998) In press
2 (bases 1 to 450)
Barak,J.D., Gilbertson,R.L. and Koike,S.T.
Direct Submission
Submitted (13-0CT-1998) Plant Pathology, University of California, Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas syringae pv. pisi.
Pseudomonas syringae pv. pisi
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
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                                                                                                                                                                                                                                                                                                                             AF098256 450 bp DNA BCT 15-NOV-1998 Pseudomonas syringae pv. pisi strain 539 internal transcribed spacer 1, complete sequence.
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S.cerevisiae DNA (cosmid 31A2; chromosome IV; 41 kb),
267750
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110 c 113 q 121 t
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Pred. No. 32;
0; Mismatches
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Pred. No. 69;
0; Mismatches
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                                                        CEVTHKTSTAAIVKTLNRNEC"
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89.5%;
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94.4%;
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Best Local Similarity 89.5
Matches 17; Conservative
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Alcohologomase, May protein, CDC3 protein; RNA helicase, STE7

Protein, Und3 protein, Masse; regulatory protein; RNA helicase, STE7

Protein, Und3 protein, Masse; regulatory protein; RNA helicase, STE7

Protein, Und3 protein

Sacharows; yeast.

WITHORS

DAILT M.

Commons of May 1179

THE CANADA CONTROLL Memiascomycetes; Saccharomycetales;

Sacharows; Commons of May 1179

THE CANADA CONTROLL Memiascomycetes; Saccharomycetales;

MARKER DAILT M.

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LRSSPVVSSFCNMYQGLPIXRSMYLHIERGISTHYNPLDRFCFWYSPRSPLFIRK
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                                                                                                                                                                                   KPKAFNVSYLSVESFEDVQKVFVRARQELSEILSAFFEMDAKSQVLAKSQLKDAAFPL
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COMPLEMENT (7252. .7764)
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ETLKKGGFLP"
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VVSTDT IKDAAACASNLTOSGIHLNAMELLDENMMKLINASESTDRCDWVEKPTMFFK
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HETCSQLVDRMVKRALNAEGTCTGEHGVGIGKREYLLEELGEAPVDLMRKIKLAIDPK
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POWY LIDKVPEDLKQVLGNKPENYSDAKSDLDAHSDTFUTHHPSPEORPRILEPHTT
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DITVQAGLPWEDLNDYLSDHGLMFGCDPGPGAGIGGCARNSCSGTNAYRYGTMKENII
                                               KLVLRPKSVEKVSLILNYCNDEKIAVVPQGGNTGLVGGSVPIFDELILSLANLNKIRD
                                                                                                                                                   3SLHGSVLGLEVVMPNGQIVNSMHSMRKDNTGYDLKQLFIGSEGTIGIITGVSILTVP
ISENYPDVHRDPRFKKLTSDDLNYFKSILSEQEILRASESEDLSFYNEDWMRKYKGQS
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14234. .15121
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complement(15246. .21683)
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FENSVSIPLEQVEPWTEIARRFASGAMSYGSISMEAHSTLAIAMNRLGAKSNGGEGGE
DAERSAVQENGDTMRSAIKQVASARFGVTSYYLSDADEIQIKIAQGAKPGEGGELPAH
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VGIVASGVAKAKADHILVSGHDGGTGAARWTSVKYAGLPWELGLAETHQTLVLNDLRR
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Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 1208)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLN
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Yeast cell division control gene CDC36.
X04287
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89.5%; Pred. No. 87;
ive 0; Mismatches
/protein_id="CAA91572.1"
/db_xref="PID:91061265"
/db_xref="GI:1061265"
/db_xref="SPTREMBL:012515"
                                                                                                                                                                                                                                                                                                                                                        complement(14650. .15129)
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CDC36 gene; cell division control.
baker's yeast.
                                                                                                                                                                                                                                                                                                                           KKKKKKKSGFFSSLKTMFN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DD 30398 TACATATGACCATTCCATG 30416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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Best Local Similarity
Matches 17; Conserv
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The direct repeat elements (1) may be implicated in the cell division cycle regulated expression of CDC9. 46 amino acids (pos. 2367-2504) show homology to regions of the T4 and T7 bacteriophage DNA ligases, and include the putative AFP binding site. CDC36 is included within the category of so-called 'start genes', encoding proteins which are required in early G1, when the cell is faced with the option of initiating a further cell cycle.

1. 3849

1. 3849

1. 3849

1. 3849
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Barker, D.G., White, J.H. and Johnston, L.H.
The nucleotide sequence of the DNA ligase gene (CDC9) from
Saccharomyces cerevisiae: a gene which is cell-cycle regulated and
induced in response to DNA damage
Nucleic Acids Res. 13 (23), 8323-8337 (1985)
                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                   10-FEB-1999
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                                                                                                                                                                                                  X03246.1 GI:3514
DNA ligase; inverted repeat; unidentified reading frame.
baker's yeast.
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                                                                                                                                   PLN
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/gene="Loco36"
/note="lmp. inverted repeat A'"
/db_xref="SGD:S0002324"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     568. :582
//gene="LDC36"
//note="imp. inverted repeat A"
//db_xref="SGD:S0002324"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="major mRNA 5' end"
/db_xref="SGD:S0002324"
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note="direct repeat 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="CDC36"
/db_xref="SGD:S0002324"
11. 3849
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/note="direct repeat 1"
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'note="direct repeat 1"
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/note="direct repeat 1"
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                                                                                                                                      Yeast CDC9 gene for DNA ligase.
X03246
                                                                                                                                                                                                                                                             Saccharomyces cerevisiae
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qene="CDC36"
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/gene="CDC36"
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/gene="CDC36"
                      272 TACATATGACCATTCCATG 290
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   2 TACATATGAGCCTTCCATG 20
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                                                                                                                                              DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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TITLE
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MEDLINE
COMMENT
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                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
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                                                                                                                SCCDC9/c
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/db_xref="SGD:394785.1"
/db_xref="PiD:93491"
/db_xref="GI:9109;93491"
/db_xref="SHID:93491"
/tanslation="MEKFRENELSTYDHSWTLGADLSSMLYSLGIP
RDSQDHRVLDTFQSRWAFTSRESPERFFPESFTNIPGYLGSTYSPPCFNSIQNDQ
RVALFQDETLFFLFYKHPGTVIQELTYLELRKRNWRYHKTLKAWLTKDPMMEPIVSAD
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Nucleotide seguence of the yeast cell division cycle start genes CDC28, CDC36, CDC37, and CDC39, and a structural analysis of the
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/codon_start=1

    1208
/organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"

                      predicted products

Wucleic Acids Res. 14 (16), 6681-6697 (1986)
86312926
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db_xref="SGD:S0002324"
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/db_xref="SGD:S0002324"
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/db_xref="SGD:S0002324"
226 c 240 g 352 t
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/db_xref="SGD:S0002324"
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Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="CAAT-like sequence"
/db_xref="SGD:S0002324"
189. 192
                                                                                                                                                                                                                                              /note="TATA-like seugence"
/db_xref="SGD:S0002324"
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/db_xref="SGD:S0002324"
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/gene="CDC36"
/note="pot. polyA signal"
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                                                                                                                                                                                                                                                                                                                                                                                                /note="pot. start codon"
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157. .160
                                                                                                                                                                                               /db_xref="SGD:S0002324"
24. .29
/gene="CDC36"
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                         77. .81
/qene="CDC36"
                                                                                                                                                                                                                                                                                                                                                              145. .147
/gene="CDC36"
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/gene="CDC36"
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/gene="CDC36"
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/gene="CDC36"
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89.5%;
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Best Local Similarity 89.5
Matches 17; Conservative
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ORIGIN
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                                                                                                                                                                 gene
                                                    JOURNAL
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/traislation="mekfglkalvplikledkelsstydhswtlgadlssmlyslgip
RDSQDHRVLDTFQSPWAETSRSEVEPRFFTPESFTNIPGVLQSTVTPPCFNSIONDQO
RVALEQDETLFFLFYKHPGTVIQELTYLELRKRNWRYHKTLKAWLTKDPMMEPIVSAD
GLSERGSYVFFDPQRWEKCQRDFLLFYNAIM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi: Ascomycota; Hemiascomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces a configuration of 2008)

Mehner, E.P., Rao, E. and Brendel, M.
Molecular structure and genetic regulation of SFA, a gene cresponsible for resistence to formaldehyde in Saccharomyces cerevisiae, and characterization of its protein product Mol. Gen. Genet. 237 (3), 351-358 (1993)
European yeast chromosome IV sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG: E-mail: Mewes@mips.embnet.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arp gene; beta-D-galactosidase; CDC36 gene; CDC9 gene; sfa gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (22-NOV-1994) E. Wehner, Institut f Mikrobiologie, Theodor Steinkai 7, Haus 75, 6000 Frankfurt/Main, FRG On Nov 28, 1994 this sequence version replaced 91:288588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-AUG-1992) E. Wehner, Institut f Mikrobiologie,
Theodor Steinkai 7, Haus 75, 6000 Frankfurt/Main, FRG
                                                                                                                                               /organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
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/strain="AH22"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SGD:S0002324"
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/db_xref="PID:4131262"
/db_xref="GI:1431262"
/db_xref="SMISS-PROT:P06100"
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Pred. No. 72;
0; Mismatches
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                                                                                                                                                                                                                                                                                            /db_xref="SGD:S0002324"
248. .823
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                                                                                                                                                                                                                                                                                                                                                                             /note="ORF YDL165w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 g
                                                                                                                                                                                                        /chromosome="IV"
248. .823
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                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                      248. .823
/gene="CDC36"
                                                                                                                                                                                                                                                                                                                       248. .823
/gene="CDC36"
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89.5%;
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Wehner, E.
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Wehner, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 c
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Best Local Similarity 89.5'
Matches 17; Conservative
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ORIGIN
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ORGANISM
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SCSFAARP/c
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                                                                                            FEATURES
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RDSQDHRVLDTFQSPWAETSRSEVEPRFFTPESFTNIPGVLQSTYTPPCFNSIQNDQO
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KNSQIKKMELIKRMITACKTEAKFLIRSLESKIGIABEKTVLISISKALLLUBDRN
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                                                                                                                                                                                                                                                                                                                                                                                                        EINITDFIODLDTTKNLILDCEAVAMDKDOGKILPFOVLSTRKRKDVELNDVKVKVCL
FAFDILCYNDERLINKSLKERREYLTKVTKVVPGEFOYATQITTNNLDELQKFLDESV
NHSCEGLMVKMLEGPESHYEPSKRSRNWLKLKKDYLEGVGDSLDLCVLGAYYGRGKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTYGGFLLĞCYNQDTGEFETCCKIGTGFSDEMLQLLHDRLTPTIDGPKATFVFDSSA
EPDVWFEPTTLFEVLTADLSLSPIYKAGSATFDKGVSLRFPRFLRIREDKGVEDATSS
DQIVELYENQSHMQN"
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sccharowyces cerevisiae
Eukaryota: Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomyceta: Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="CDC36"
/note="open reading frame (CDC36) (aa 1-191)"
/codon_start=1
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3142. .3144
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/db_xref="$GD:$0002324"
755 c 771 q 1158 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SGD:S0002324"
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/gene="CDC36"
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2 (bases 1 to 944)
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Best Local Similarity
Matches 17; Conserv
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JOURNAL
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TITLE
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Gaps

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Length 944; 2; Indels 29-NOV-1994

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Comp.esm...,
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ATFDKGVSLRFPIFLRIREDKGVEDATSSDQIVELYENQSHMQN"
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                                                 /gene="CDC9"
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BASE COUNT ORIGIN

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 79.0%; Score 15.8; DB 8; Length 7008; 89.5%; Pred. No. 79;
                                    Indels
                                    0; Mismatches
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Job time: 1466 sec
                                                                                        1075 TACATATGACCATTCCATG 1057
                                                                   2 TACATATGAGCCTTCCATG 20
Query Match 79.0°
Best Local Similarity 89.5
Matches 17; Conservative
                                                                     ò
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us-09-037-472-10.rng

Page

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: September 18, 1999, 05:27:26; Search time 213.04 Seconds

(without alignments)
23.488 Million cell updates/sec

tle: US-09-037-472-10 rfect score: 20

Perfect score: 20 Sequence: 1 TTACATATGAGCCTTCCATG 20

Scoring table: IDENTITY\_NUC

Searched: 311585 segs, 125096042 residues

N\_Geneseq\_36:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	2000	11771011	for de	eukin-1-	eukin 1	IL-1ra	rO	acety	in SP	S E	tis E	ssed Sequence	Human brain Expres	ud sno	primer used to	itrat	citrate	itrate s	~		papillom	Poly	Tryptophan-2,3-dio	44	Human immunodefici	Wasp Brh-1 toxin g	ı papillomavir	occus furiosu		O,	-	papilloma	dney cel	iral	dney calci	sequence i	μį			.da neoformans	Staphylococcus aur	parathyroid ca	W	semaphorin r	Ŋ
	5	7000	Primer	Interl	Interl	Нишап	Urea		HEV :	Hepatiti	Hepati	Expres	Huma	Stre	PCR	Potato	Tobacco	Pota	Cont	Cont	Human	Brh-I	Tryp	Rat	Huma	Wasp	Huma	Pyro		DNA	Ниша	~			Rat	Target	Ehrlichi	Candida	Candida	Candida	Stap	Rat	Mous	Mouse	Mouse
SUMMARIES	Ę		138	2	99	88	9460	24	519	T27394	160	Q39643	902	V52144	V42902	T04199	T04201	T03410		V30459_1	Q25937	Q48438	089299	085956	T36179	T45675	T44713	T62078	T78149	T87040	T88023	T91251	T95860	V20488	V26965	V37216	v07180	V33683	V33681	V33682	V78075	V82486	x08997	x08998	66680 <b>x</b>
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Mouse semaphorin r
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Transcription of increased periodontal disease by
Transcription of the persence of DNA polymorphisms in the gene sequences
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Transcription of the persence of DNA from a blood or tissue sample and products are used
Transcription of the persence of the persence of the patient. A single base variation (C/T) polymorphism
Transcription of the persence of dentified using primers (T70316 and
Transcription of the persence of the persence of dentified using primers (T70316 and
Transcription of the persence of the pers
                        DNA encoding P30a
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                                                                                                                                                                                                                                                                                             Primer for detecting genetic predisposition to periodontal disease. Primer for detecting genetic predisposition to periodontal disease; gingivitis; periodontitis; polymorphism; interleukin-1 alpha; IL-1A; interleukin-1 beta; IL-1B; primer; PCR; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                         ALIGNMENTS
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10-OCT-1997; G02790.

10-OCT-1996; GB-021129.

(DUFF) DUFF G.

(RICH) REUNIE I.

(RICH) RICHARDSON R.

Duff G. REDNIE I, RICHARDSON R;

WPI: 98-240835/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-1997.
02-AUG-1996: U12455.
03-AUG-1995: US-510696.
(RORN/) KORNMAN K S.
(MEDI-) MEDICAL SCI SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TTACATATGAGCCTTCCATG 20
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                                                                                                                                                                                                                                  T13884 standard; DNA; 20 BP. T13884;
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but not if T is present.
Sequence 20 BP; 5 A;
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WPI; 97-154207/14.
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71.0
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WO9815653-Al.
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V32396
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James 2, Page 33; 41pp; English.

Claim 2, Page 33; 41pp; English.

Interleukin 1-alpha (IL-1-alpha) primers 4 and 3 (V32395) were used to maplify the IL-1-alpha gene region to identify single base variation polymorphism of CT at base 889. The invention claims to provide a nethod for predicting the risk of sight threatening diabetic retinopathy.

The method involves isolating DNA from a patient and determining the DNA polymorphism pattern of the genes that code for interleukin-1-alpha, interleukin-1-bet and interleukin-1-RN. The polymorphic pattern interleukin-1-bet and interleukin-1-RN. The polymorphism pattern thereby identifying patients carrying a genetic polymorphism pattern thereby identifying patients carrying a genetic polymorphism pattern thereby identifying patients carrying a genetic polymorphism pattern associated with increased risk of sight threatening diabetic retinopathy. The method may be able to identify diabetic patients at risk before the clinically detectable disorders occur. Polymorphism pattern clinically detectable disorders occur. Polymorphism pattern of IL genes involved PCR reactions using primers v32389-v32398. The method is also claimed to be useful in conjunction with incremination of IL genes involved PCR reactions using primers v32389-v32398. The method is also claimed to be useful in conjunction with certinication of other genes associated with sight threatening diabetic patients expressing multiple risk patterns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COXA) COX A.

A (DOIV) DE GIOVINE F S.

A (DOIV) DE GIOVINE F S.

A (DOIF) DE GIOVINE F S.

A (DUFF) DUFF G.

B (DUFF) DUFF G.

A (DUFF) D
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Interleukin 1 (44112332) haplotype PCR primer #6.
Interleukin 1: IL-1; haplotype; inflammatory disorder; alopecia areata; coronary artery disease; osteoporosis; nephropathy; diabetes mellitus; Graves disease; systemic lupus erythamatosus; lichen sclerosis; ulcerative colitis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Predicting increased risk of sight-threatening diabetic retinopathy - comprises identifying genetic polymorphism pattern for genes IL-1A, IL-1B and IL-1RN, useful to allow treatment before clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Best Local Similarity 100.
Matches 20; Conservative
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21-MAY-1998; G01481.
29-MAY-1997; GB-011040.
(CAMP/) CAMP N J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
WO9854359-Al.
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WPI; 99-153692/13.

New isolated nucleic acid encoding the new human cytokine Tango-77 - used to inhibit inflammation and to screen for specific modulators

Example 5: Figure 3: 226pp; English.

X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

CC X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

CC Tango and the method of the invention which describes the isolation of a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a inflammation by binding to the interleukin-1 receptor (IL-1R). It may also bind to a new receptor so could requilate other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic conflammation are acid inflammatory bowel disease. It may also induce or suppress interleukins, cytokines and growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of inflammation, or activity
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disease-associated haplotype enables determination of which alleles are causative, and this information is useful in designing treatment strategies, including gene therapy and treatment using various agents that modulate the activity of proteins produced by the IL-1 gene cluster some alleles from the IL-1 gene cluster are associated with particular inflammatory diseases, and insufficient IL-1 production appears to act gene clusters is useful in determining genetic susceptibility to inflammatory diseases, including those with a multifactorial etiology with a polygenic component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-1999 (first entry)

Human IL-Ira BAC contiguous DNA sequence 33.

Hango-7: human; IL-Ira, cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-IR; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                                                                                                                          Gaps
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03-AUG-1998: (16102.
03-AUG-1999: US-091650.
04-AUG-1997; US-054646.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
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5701 BP; 1729 A;
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Best Local Similarity
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Best Local Similarity
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Gaps

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Purified hepatitis E strain SAR-55 virus - used to develop prods. for use in detection, diagnosis, vaccines and therapy of hepatitis E virus infection Claim 2; Page 16-20; 114pp; English. This sequence represents the genomic sequence of the hepatitis E virus (HEV) strain SAR-55. This sequence contains three open reading
                                            New peptide(s) useful in treatment of myasthenia gravis - also in diagnosis, having acetyl:choline receptor-alpha like activities. Disclosure; Fig 1; 13pp; Japanese.
Peptides derived from the hACR-alpha gene product have similar immunogenicity to the gene product, and may be useful in the treatment and diagnosis of myasthenia gravis caused by neuropathy in autoimmune reaction to ACR.
The sequence given contains breaks in some of the introns, at these locations 60 N residues have been inserted to preserve integrity.
Sequence 4708 BP; 1124 A; 1059 C; 965 G; 1200 T;
                                                                                                                                                                                                                                                                                                                                   045197 standard; CDNA; 7168 BP.
045197;
21-0CT-1994 (first entry)
HEV strain SAR-55 CDNA sequence.
HEPAILLIS E VIRUS; HEV; Strain SAR-55; open reading frame; ORF; antibody; detection; diagnosis; primates; stool suspension; ss.
Hepailtis E virus strain SAR-55.
                                                                                                                                                                                                 Length 4708;
                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                  DB 1;
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31-MAR-1594.
17-SEP-1994.
18-SEP-1992; UG849.
18-SEP-1992; US-947263.
(USSH ) US SEC DEPT HEALTH.
Emerson SU, Purcell RH, Tsarev SA;
WPI; 94-118462/14.
P-PSDB; R51264-66.
Purified hepatitis E strain SAR-55 virus - 1
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                                                                                                                                                                                                                19;
                                                                                                                                                                                                  79.0%; Score 15.8; 89.5%; Pred. No. 19
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misc_difference 3757. 3759
/*tag= c
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misc_difference 5011. .5013
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28. .5109
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misc_difference 4081. .4083
/*tag= d
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5147. .7129
/*tag= f
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05-0CT-1983; JP-186402.
(MITU) MITSUBISHI CHEM IND KK.
WPI: 85-144120/24.
P-PSDB; PSO561.
                                                                                                                                                                                                                                                                                                                                                                                                                                              cus /*tag= a //tabel= ORF-1 misc_difference 3739. .3741 /*tag= b
                                                                                                                                                                                                                                                                  1164 TGACAGATGAGCCTTCCAT 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= ORF-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5780. .5782
/*tag= 9
                                                                                                                                                                                                                                                  1 TTACATATGAGCCTTCCAT 19
                                                                                                                                                                                                              Best_Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_differerce
                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                               RESULT
Q45197
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                                                                                                                                                                                                            from Saccharomyces yeast - can be used to prepare high purity urea amidolyase by culturing the transformant comprising the DNA claim 1; Page 10-17; 17pp; Japanese.
This sequence encodes a protein which has urea amidolyase (URL) - activity and is derived from yeast. This sequence may be used within a recombinant plasmid from the production of highly pure URL sequence 6265 BP; 1873 A; 1156 C; 1361 G; 1875 T;
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                           (TOYM ) TOYOBO KK.
WPI; 93-38925/43.
P-55DB; R42839.
DNA having the genetic information of urea amidolyase originated
                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                         82.0%; Score 16.4; DB 1; Length 6265; 94.4%; Pred. No. 9.2; 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human acetyl choline recéptor alpha gene.
hACR-alpha; myasthenia gravis; MG; neuromyopathy; ds.
                      Urea amidolyase gene.
Urea amidolyase; URL; yeast; recombinant plasmid; ss.
Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89. 328
/*tag= c
/note= "60N inserted as a spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inserted as spacer"
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/note= "60N inserted
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                                                          Location/Qualifiers
627. .6134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N50415 standard; DNA; 4708 BP. N50415;
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2671. .2994
/*tag= j
                                                                                                /product= URL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-1992 (first entry)
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89. .328
              (first entry)
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/*tag=
346. .3;
                                                                                                                         24-SEP-1993.
05-MAR-1992; 084531.
05-MAR-1992; JP-084531.
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1863. .
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05-0CT-1983; 186402.
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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          0-MAY-1994
                                                                                                             J05244959-A
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us-09-037-472-10.rng

following SDS-PAGE of cell lysates of insect cells infected with a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant expression vectors pPIC9-1779, -1780 and -1781. Sequence 7158 BP; 1221 A; 2293 C; 1864 G; 1780 T;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tisolated and purified hepatitis E virus strain SAR-55 DNA - encodes antigenic protein useful in diagnosis, prophylaxis and treatment of antigenic protein useful in diagnosis, prophylaxis and treatment of antigenic protein useful in diagnosis, prophylaxis and treatment of Claim 2: Pages 16-21; 121pp; English.

Claim 2: Pages 16-21; 121pp; English.

The present sequence is the CDNA of the hepatitis E virus (HEV)

Strain SAR-55, which was implicated in an enterically transmitted non-A, non-B hepatitis in Pakistan. The protein encoded by the con-A, non-B hepatitis in Pakistan. The protein of HEV structural region of the virus (i.e. ORF-2), which is capable of structural region of the virus (i.e. ORF-2), which is capable of forming HEV like particles, is useful for the detection of HEV cerebrospinal fluid, tissue, urine or pleural fluid. The protein, can antibodies generated using the protein, can also be used in vaccines for immunising an animal against HEV infection.

The protein is identified as a band of greater than 50 kD
frames (ORFs). The proteins encoded by this sequence can be used to stimulate the production of protective antibodies upon injection into a mammal that would serve to protect the mammal upon challenge with wild type HEV. The proteins can be used for detection and diagnosis of HEV infection. This cDNA was isolated from primates innoculated with stool suspensions obtained [2294 C, 1867 G, 1784 T;
                                                                                                                                                                                                                           Gaps
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/note- "10 bp nucleic acid sequence TGGTNTTYGA
as to be inserted between nucleotides
4390. .4391 for numbering to conform to
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/note= "10 bp nucleic acid sequence TGGTNTTYGA
has to be inserted between nucleotides
4390. 4391 for numbering to conform to
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/note= "10 bp nucleic acid sequence TGGTNTTYGA
has to be inserted between nucleotides
4390. 4391 for numbering to conform to
                                                                                                                                                                                                                                                                                                                                                                                                 T27394 standard; CDNA; 7158 BP.
T27394;
26-NOV-1996 (first entry)
Hepatitis E virus strain SAR-55 cDNA (ATCC 75302).
Hepatitis E virus; HEV; SAR-55 strain; enteric transmission; structural region; antigen; detection; antibody; vaccine; immunisation; infection; ss.
Location/Qualifiers
Key
                                                                                                                                                                                 Length 7168
                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                              79.0%; Score 15.8; DB 1; 89.5%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that given in the specification" 5096. .5467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    that given in the specification'
5137. .7119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that given in the specification
                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-0CT-1995; U13102.

03-0CT-1994; US-316765.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Emerson SU, Purcell RH, Tsarev SA;

WPI; 96-209320/21.

P-PSDB; R91813, R91814, R91815.
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/label= ORF-1 (R91813)
                                                                                                                                                                                                                                                                                                    2189 TTACATCTGAGCCTTCTAT 2207
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                                                                                                                                                                                                      Best Local Similarity
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                  Gaps
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  Length 7158;
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                                                                                                                                                                          .3741, aa:Glu)
.3759, aa:Glu)
.4083, aa:Glu)
.5013, aa:Glu)
                                                                                                                                                                                                                                 /transl_except= (pos:5780. .5782, aa:Tyr)
                  Indels
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Score 15.8; DE
Pred. No. 19;
0; Mismatches
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Pred. No. 19;
0; Mismatches
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/transl_except= (pos:3739.
                                                                                                                                                                                                                                          /product= "ORF-2 protein"
                                                                                                                                                                                                                                                                 /product= "ORF-3 protein"
                                                                                                                                                                                                                                                                                    ZZ-OCI-1998.
09-APR-1997; US-840316.
11.APR-1997; US-840316.
(USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                  Location/Qualifiers
28. .5109
                 ö
                                         2189 TTACATCTGAGCCTTCTAT 2207
                                                                                        V71604 standard; DNA; 7168 BP
79.0%;
89.5%;
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                                1 TTACATATGAGCCTTCCAT 19
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                                                                                                         (first entry)
Query Match 79.0
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                passive immunisation; ss.
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Best Local Similarity 89.5'
Matches 17; Conservative
                                                                                                                                                                                                                          /*tag=
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                                                                                                                                          Hepatitis E virus.
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                                                                                                        02-FEB-1999
                                                                                                  V71604;
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coding-region prediction program CRM. Sequence 354 Bp; 123 A; 61 C;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Particular expressed sequence tags from human CDNA - corresponds

To transcription prods. of genes, useful for tagging genes,
mapping chromosomes and tissue typing

To transcription prods. of genes, useful for tagging genes,
mapping chromosomes and tissue typing

State of 199pp; English.

This sequence represents an EST (expressed sequence tag) ESTs are markers

for human genes actually transcribed in vivo. Unlike the random genomic

DNA sequence ragged sites (STSs), ESTs point directly to expressed genes.

The use of ESTs could facilitate the tagging of most expressed human

genes within a few years at a fraction of the cost of complete genomic

Sequencing. Using PCR primers 039419-039580 (sequences designed

from the ESTs) sublocalisation of an EST can be achieved with panels of
fragments from specific chromosomes or pools of large genomic clones in

an analogous manner. This sequence represents EST00020.

Sequence 354 BP; 126 A; 62 C; 90 G; 70 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Example 1; Page 114; 500pp; English.

The Expressed Sequence Tag was isolated from a human brain cDNA
library as part of a large set of ESTs which can be used as markers
for human genes transcribed in two. They can be used to facilitate
tagging of most human genes, for mapping locations of expressed genes
on chramosomes, for individual or forensic identification, for mapping
locations of disease-associated genes, for identification of tissue
type, and for prepn. of antisense sequences, probes and constructs.
EST00020 has an "excellent" coding probability as evaluated using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Gene transcription product; genetic markers; tagging; in vivo;
transcription; mapping; locations; chromosomes; chromosomal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 93-272882/34.
Enriched oligonucleotides and corresp. sequences - used as
markers for human genes transcribed in-vivo, facilitate tagging
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                                                                                                                                                                                                                                       Expressed Sequence Tag human gene marker EST00020. expressed sequence tag; human genome project; chromosome; human gene sequencing; PCR mapping; somatic cell hybrids; sublocalisation; gene tagging; tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JAN-1993.
19-JUN-1992. U05222.
20-JUN-1991. US-716831.
12-FEB-1992. US-837195.
(USSH ) US DEPT HEALTH & HUMAN SERVICE.
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12-FEB-1993; U0-837195.
(USSH ) US DEPT HEALTH & HUMAN SERVICE.
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ID Q59055 standard; cDNA; 354 BP.
                                                                                                                                 Q39643 standard; DNA; 354 BP
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                                                                                                                                                                                                     20-MAY-1993 (first entry)
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Best Local Similarity 85.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter JC;
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WO9316178-A
                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
WO9300353-A.
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The present invention describes a computer readable medium which has the present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded on it, or a representative fragment or a sequence at least 95% identical CC to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae GC molecule encoding a homologue of any of the fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a cc probe a target sequence defined by any of the sequences in SEQ ID NO:1 that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mencles from the members; or (c) isolating mencles from the members; or (b) isolating mencles from the computer readable medium can be sequence is homologous to amplification primers derived from the computer-based system for identifying fragments of the S. pneumoniae genome to prime the amplification and cused in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present fragments of the S. pneumoniae genome. Products from the present for invention can be used in diagnosis kits and assays, and pharmaceutical commonsitions and vancines for a monomonial for a manimum tand.
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31-OCT-1995; US-029960.
31-OCT-1995; US-029960.
HUMA-) HUMAN GENONE SCI INC.
Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M,
Kunsch CA, Rosen CA;
WPI: 98-27225/24.
Computer-readable medium with recorded Streptococcus pneumoniae
polynucleotide sequences - useful in diagnostic kits and assays, and
pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Streptococcus pneumoniae genome fragment SEQ ID NO:11.
Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
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See also Q59041-Q61440.
92 G: 70 T:
                                                                                                                                       Length 354;
                                                                                                                                                                                                            3; Indels
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                                                                                                                                       DB
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                                                                                                                                                                                                         0; Mismatches
                                                                                                                                   76.0%; Score 15.2; 85.0%; Pred. No. 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V52144 standard; DNA; 8148 BP.
                                                                                                                                                                                                                                                                           1 TIACATATGAGCCTTCCATG 20
                                                                                                                                                                                                                                                                                                                                            62 TITCACAIGAACCTICCAIG 43
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                                                                                                                                                                                                         17; Conservative
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Best Local Similarity 85.0°
Matches 17; Conservative
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W09818931-A2.
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Sequence
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          888888
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Example 1; Page 
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To identify a cDNA from potato which codes for citrate synthase, a cDNA fragment of citrate synthase from Arabidopsis thaliana was firstly amplified using A.thaliana cDNA and oligos T04202 and T04203 which are complementary to the 5' or 3' end of the coding region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Targeting adenovirus to cell-surface protein - using bifunctional ligand that interacts with adenovirus fibre and cell-surface protein
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22-oCT<sub>0</sub>1998 (first entry)
PCR primer used to mutate part of graph adenovirus serotype 5.
Domain alpha 2; antigen; major hi-tocompatibility complex class I;
MHC-I; primary receptor; serctype G adronovirus; human; fibronectin;
module III; targeting; cell-surface rotein; cellular receptor;
bifunctional ligand; tumour cell; intected cell; PCR primer; ss.
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Mueller-roeber B;
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Potato citrate synthase cDNA.
Citrate synthase; flower formation; tuber storage; ss.
Solanum tuberosum.
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85.0%; Pred. No. 22;
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09-MAR-1994; DE-408629.
22-2EP-1994; DE-4386.
19-CCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
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73. .1485
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09-SEP-1997; 011166.
30-JAN-1997; FR-001005.
(CNRS ) CNRS CENT NAT RECH SCI.
Boulanger P, Hong SS, Karayan L;
WPI; 98-416459/36.
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/*tag= a
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                Māstadenovirus.
FR2758822-A1.
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                                                                                                                                                                                                                               Gaps
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A. thaliana cDNA for citrate synthase. The oligos additionally introduce BamHI cleavage sites at both ends of the amplified cDNA fragment. a cDNA library was prepd. from potato leaves and screened with A. thaliana citrate synthase cDNA. Positive clones were purified and sequenced. Then t sequence is given in T04199. Sequence 1891 BP; 512 A; 370 C; 425 G; 584 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  La Cognata U, Landschutze V, Muller-rober B, Landschuetze V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to improve storage of tubers, etc. and to reduce sprouting Claim 7: Page 60-63: 87pp; English.
To identify a cDNA from tobacco which codes for citrate synthase, a cDNA bank of leaf tissue from tobacco was prepd. Plaques of this cDNA bank were screened using a radioactive DN probe which comprises Solanum tuberosum citrate synthase cDNA.
                                                                                                                                                                                   Length 1891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1747;
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                                                                                                                                                                                   Score 14.8;
Pred. No. 56;
                                                                                                                                                                                                                               Mismatches
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Job time: 1692 sec
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Tobacco citrate synthase cDNA.
Citrate synthase; flower formation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                T04201 standard; cDNA to mRNA; 1747 BP.
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19-OCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
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                                                                                                                                                                                   74.0%;
88.9%;
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88.9%;
                                                                                                                                                                                                                                                                                                688 ACATAIGAGGATTCCATG 705
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                                                                                                                                                                                Query Match 74.0
Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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07-MAR-1995;
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06:47:49; Search time 1405 Seconds (without alignments) 28.079 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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                                                                                     nucleic search, using sw model
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                                                                                                                              September 18, 1999,
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Perfect score:
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                                                                                       nucleic
                                                                                                                                                                                                                                                               Sequence:
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                                                                                                                                 Run on:
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R19433 yg25c03.r1
D55860 HUM404C08B
AA831249 oc73e01.s
AA130847 oc73e01.s
A130847 qc14a10.x
A130847 qc14a10.x
A130847 qc14a10.x
A120847 qc14a10.x
D5228 HUM0106D02B
H90734 yv20a11.s1
AA17255 HUM0106D02B
H95844 yv20a11.s1
AA276311 vc06a11.r
AA276311 vc06a11.r
AA276311 vc06a11.r
AA3777 vc06a11.r
AA3777 vc06a11.r
AA48850 ny77a08.s
AA70389 vv04a06.r
AA78850 ny77a08.s
AA70389 vv04a06.r
AA48850 ny77a08.s
AA70389 vv04a06.r
AA66883 vx15d06.r
AA66883 vx15d06.r
AA401166 cu51e04.r
AA401166 cu51e04.r
AA401165 ym24c02.r1
R66347 yi34f00.s1
H8272 yr24d06.s1
H82720 yv81c02.s1
H82720 yv81c02.s1
H82720 yv81c02.s1
N6516 yy4d06.s1
AA126072 s15d03.r
AA126072 s15d03.r
AA126072 s15d03.r
AA126072 s15d03.r
AA126072 s10b12.r
                                                                                                                                                                                                                                                                                                                    AA442950 zx73e12.r
AA069310 AU069310
                                Pred. No. is the number of results predicted by chance to have a score greater than or equal, to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                        Description
                                                       SUMMARIES
                                                                                R19433
D55860
AA831249
AA908884
AII30847
AII30847
AII30847
AII30847
AAI97351
AAA197351
AAA288092
                                                                                                                                                                                                  H78857
AA401166
D46229
H08527
H14725
H14725
H14725
H14725
H2720
H82720
N46516
AA126072
AA126072
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AA126072
AA136072
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AA673147
AA748850
AA790389
AA863883
AI226166
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em_est22:*
em_est23:*
em_est24:*
em_est25:*
em_est26:*
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Match
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58:
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R19433 407 bp mRNA EST 14-ApR-1995 yg25c03.rl Soares infant brain INIB Homo sapiens cDNA clone IMAGE:33575 5', mRNA sequence. R19433 g773043 R19433.1 G1:773043

DEFINITION

RESULT 1 R19433/c LOCUS

ACCESSION NID VERSION

ALIGNMENTS

Nagata, M.,

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N29325 476 bp mRNA EST 05-JAN-1996
yw84c11.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
clone IMAGE:258932 3', mRNA sequence.
                                                                                                                                                               Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
High quality sequence stops: 278
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 278.

Location/Qualifiers
1. 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 476)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Naga Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
Fujiwara et al. (1995)
Unpublished (1995)
On Sep 21, 1992 this sequence version replaced gi:279304.
                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="ilb="Clontech human fetal brain polyA+ mRNA (#6535)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
On May 18, 1995 this sequence version replaced gi:810971
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
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High quality sequence stop: 353.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.0%; Score 16.8; 90.0%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152
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Fax: 314 286 1810
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Best Local Similarity
Matches 18; Conserv
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91147845
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                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 2026
High quality sequence stops: 228 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D55860 360 bp mRNA EST 31-AUG-1995
HUM404C08B Clontech human fetal brain polya+ mRNA (#6535) Homo
sapiens cDNA clone GEN-404C08 5', mRNA sequence.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 360)
                                                                                                1 (bases 1 to 407)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="CDB:405922"
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/clone="IMAGE:33575"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 228
Location/Qualifiers
1. .407
                                                                                                                                                                                                                        The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.0%;
94.7%;
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D55860.1 GI:970260
                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                         Homo sapiens
                                                                                                                                                                                                     Wilson, R.
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  EST.
human.
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SOURCE
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Gaps

Sep

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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Trissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert_Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA908884 493 bp mRNA EST 23-JUN-1998 om51f02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1550715 3' similar to SW:YNBH_YEAST P53729 HYPOTHETICAL 48.1 KD PROTEIN IN SEC12-SSK2 INTERGENIC REGION. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 493)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:1550715"
/clone_lib="NCI_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host=="BH108"
/note="Vector: pI773D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                   constructed by Bento Soares and M. Fatima Bonaldo."
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Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:2044779.
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                                                                                                                                                                                                                                                                                                                                                                Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
     /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                            84.0%; Score 16.8; DB 39;
90.0%; Pred. No. 36;
live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 467.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  www-bio.llnī.gov/bbrp/image/image.html
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/db_xref="taxon:9606"
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AA908884.1 GI:3048289
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Best Local Similarity
Matches 18; Conserv
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGPP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA831249 488 bp mRNA EST 21-APR-1998 cor3ed1.21 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1355352 3/ similar to SW:YN8H_YEAST P53729 HYPOTHETICAL 48.1 KD PROTEIN IN SEC12-SSK2 INTERGENIC REGION: ;, mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2285618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
__CDNA_Library_Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 373.
Location/Qualifiers
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Pred. No. 36;
0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:1355352"
/clone_lib="NCI_CGAP_GCB1"
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90.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                         AI130847 598 bp mRNA EST 27-OCT-1998 qc14a10.xl Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone IMAGE:1709562 3' Similar to SW:YNBH_YEAST P53729 HYPOTHETICAL 48.1 KD PROTEIN IN SEC12-SSK2 INTERGENIC REGION.; mRNA sequence. AI130847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 598) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@lih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@limage.llnl.gov) for further information. Insert Length: 771 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality. sequence stop: 440.
polylinker; 1st strand cDNA was prepared from 3 pooled
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Unpublished (1997)
On Jan 9, 1998 this sequence version replaced gi:930548
                                                                                                                                                                                            Length 493;
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/organism="homo sapiens"
/do_xre="taxon:9606"
/clone="IMAGE:1709562"
/clone_lib="Soares_fetal_heart_NbHH19W"
                                                                                                                                                                                            DB 40;
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                                                                                                                                                                                            84.0%; Score 16.8; D 90.0%; Pred. No. 36; iive 0; Mismatches
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AI130847.1 GI:3600863
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Best Local Similarity 90.0
Matches 18; Conservative
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                                                                                                                       BASE COUNT
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1 others

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88 9

211

BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Email: Robert_Strausbergenih.gov
This Clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.llnn.gov) for further information.
Insert Length: 772 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stope: 354.
Location/Qualifiers
I. 567
/ Organism-"Homo sapiens"
//db_xref="taxon: 9606"
//db_xref="taxon: 9606"
//db_xref="taxon: 9606"
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                                                                                                                                                                                                                                                                                                                                                              Homo saplens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 567)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                     Gaps
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2151692.
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/sex-"male"
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Length 598;
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 DB 42;
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90.0%; Pred. No. 36;
live 0; Mismatches
 Score 16.8; D
Pred. No. 37;
0; Mismatches
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84.0%;
90.0%;
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                                                                                            30 TIACATATGAGACTITCATG 99
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Best Local Similarity 90.0
Matches 18; Conservative
                                     Conservative
 Query Match
Best Local Similarity
Matches 18; Conserv
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Gaps

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H90734 28-NOV-1995 WRNA EST 28-NOV-1995 yu84a04.sl Soares fetal liver spleen INFLS Homo sapiens CDNA clone IMAGE:240462 3' similar to contains Alu repetitive element;, mRNA
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kaqasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estewatson.wustl.edu
Insert Size: 809
High quality sequence stops: 369
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 809 Std Error: 0.00
Seq primer: Promega -21ml3
High quality.sequence stop: 369.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo.

(bases I to 447)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                       /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/db_xref="CEN-106D02"
/clone="Ib="Clontech human fetal brain polyA+ mRNA (#6535)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:838025
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/db_xref="taxon:9606"
/clone="IMAGE:240462"
/sclone="lib="Soares fetal liver spleen lNFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                  Length 402;
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/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Had Vase Park Parkway, Box 8501, St. Louis, MO (
Tel: 314 286 1810
Fax: 314 286 1810
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85.0%; Pred. No. 59;
iive 1; Mismatches
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                                                                                                                  Location/Qualifiers
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The WashU-Merck EST Project
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H90734.1 GI:1081164
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Best Local Similarity 85.0
Matches 17; Conservative
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JOURNAL
COMMENT
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Eutheria; Primates; Catarrhin; Hominidae; Homo.

( bases 1 to 402)

Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinoniya, H., Takaichi, A., Takeda, S., Matanabe, T., Takahashi, E., Hirai, Y., Fujiwara et al. (1995)

Unpublished (1995)
                                                                                                                                                                                                                                      Homo sapiens
Homo sapiens
Homo sapiens

Eutharyota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutharia: Primates: Ctarrhini; Hominidae; Homo.

1 (bases 1 to 379)

2 (bases 1 to 379)

3 (bases 1 to 379)

3 (bases 1 to 379)

4 (bases 1 to 379)

5 (bases 1 to 379)

6 (bases 1 to 379)

7 (bases 1 to 379)

8 (base 1 to 379)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D53341 402 bp mRNA EST 19-SEP-1995 HUM106D02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens CDNA clone GEN-106D02 5', mRNA sequence.
                                                   D52258 379 bp mRNA EST 14-SEP-1995
HUM072G05B Clontech human fetal brain polyA+ mRNA (*6535) Homo
sapiens cDNA clone GEN-072G05 5', mRNA sequence.
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/db_xref="taxon:9606"
/clone="GEN-072605"
(*clone="lib="Clontech human fetal brain polyA+ mRNA (*6535)"
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On May 8, 1995 this sequence version replaced gi:801457
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High quality sequence stop: 328.
Location/Qualifiers
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85.0%; Pred. No. 58;
iive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 TTACATATGAGGCTKTCATG 295
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D53341.1 GI:955238
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                                                                                                                                                     9952494
D52258.1 GI:952494
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D53341/c
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D52258/c
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SOURCE
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296 TACATTTGAGGCTTCCATG 278
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                                                                                                                                                                                                                                                                                                   mRNA sequence.
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                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                        H95824 424 bp mRNA EST 25-NOV-1996
yv20all.sl Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:243260 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7441 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 114 286 1810
Fax: 314 286 1810
Finity sequence stops: 315
Source: InAgE Consortium, LLNL
This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image-llnl.gov) for further information.
Insert Length: 804 Std Error: 0.00
Seq primer: m13 -40 forward.
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        To (bases 1 to 424)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rikkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Washu-Merck EST Project
Unpublished (1995)
On Jan 25, 1995 this sequence version replaced gi:637882
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/db_xref="GDB:3792393"
/db_xref="taxon:9606"
/clone="IMAGE:243260"
/sex="male"
                                                                                                                                                                                             Length 447;
                                                                                                                                                                                              Score 15.8; DB 24; Length
Pred. No. 1.2e+02;
); Mismatches 2; Indels
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                                                                                                                                                                                             79.0%; Scor
89.5%; Pre-
                                                                                                                                                                                                                                                                          280 TACATTTGAGGCTTCCATG 262
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H95824.1 GI:1108966
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H95824/c
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KEYWORDS
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SOURCE

LOCUS

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3']; double-stranded cDNA was ligated to Eco RI adaptors Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr713 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatian Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 630) Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA197351 630 bp mRNA EST 19-FEB-1997 mu21e06.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:640066 5',
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WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseset@watson.wustl.edu
This clone is available royalry-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
      Library
                                                                                                                                                                                                                                                                   Gaps
and Eco RI sites of the modified pT/T3 vector. Lik went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo." 87 e 94 g 117 t 1 others
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On Sep 12, 1996 this sequence version replaced gi:1393441.
                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                         Length 424;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                      ch 79.0%; Score 15.8; DB 24;
1 Similarity 89.5%; Pred. No. 1.2e+02;
17; Conservative 0; Mismatches 2;
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Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 507.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C55BL/6J"
/db_xref="taxon:10090"
/clone="InAGE:640066"
/clone=lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 427)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA275311 427 bp mRNA EST 31-MAR-1997 vc06a11.rl Soares mouse lymph node NbMLN Mus musculus cDNA clone IMAGE:765692 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
HashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Eax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:466612
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
On Nov 29, 1993 this sequence version replaced gi:430191.
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                                                                                     Score 15.8; DB 30; Length 630;
Pred. No. 1.2e+02;
0; Mismatches 2; Indels 0
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| Sub_xref="taxon:10090" | Clone="IMAGE:76562" | Clone_lib="Soares mouse lymph node NbMLN" 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative full length read
vector to vector length is 627
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 406.
Location/Qualifiers
1. 427
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.
The WashU-HHMI Mouse EST Project
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AA275311.1 GI:1915708
                                                                                             79.0%;
89.5%;
                                                                                                                                                                                                                                                                                            207 TAGATCTGAGCCTTCCATG 225
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                                                                                                                                                                                                                                                     2 TACATATGAGCCTTCCATG 20
                                                                                                                                        al Similarity 89.5
17; Conservative
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                                                                                                     Query Match
Best Local
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AUTHORS
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ORIGIN
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_"IMAGE_748913"
/clone_"IMAGE_748913"
/clone_"IMAGE_748913"
/clone_"IMAGE_748913"
/clone_"IMAGE_748913"
/lab_host="DHIOB"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
/note="Vector: pT73D-Pac (Pharmacia) with a modified pT773 wector: Library
and Eco RI sites of the modified pT773 vector: Library
constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Bukaryota; Metazoa; Chordata; Craniata; Wurinae; Mus.

1 (bases 1 to 432)

1 (bases 1 to 432)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schptoe, M., Tan, F., Underwood, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The Washu-HHM Mouse EST Project
Unpublished (1996)

On Sep 12, 1996 this sequence version replaced gi:1397406.
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                                                                                                                                                                                                                                                                                                                     AA288092 432 bp mRNA EST 11-APR-1997 vb14d09.rl Soares mouse NML Mus musculus cDNA clone IMAGE:748913
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                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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     Length 427;
                                                              Indels
Score 15.8; DB 31;
Pred. No. 1.2e+02;
0; Mismatches 2;
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High quality sequence stop: 406.
Location/Qualifiers
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Mus musculus
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Indumentary Primates; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

RS Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields C. and Venter,J.C.

Rapid Corba Sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library

Nature Genet. 4, 373-380 (1993)

On Sep 12, 1996 this sequence version replaced gi:1288980.

On Sep 12, 1996 this sequence version replaced gi:1288980.

Other_ESTS: EST89819 THC137556

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Restarch

9712 Medical Center Drive, R.ckville, MD 20850 USA

Tel: 30186999423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13-21.
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/db_xref="ATCC (inhost):181679"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dov_stage="small intestine II"
/dev_stage="adult"
/note="corgan: small intestine; Vector: pBluescript SK-;
site_I: ECORI; Site_2: XhoI" 3 others
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                                             AA377278 372 bp mRNA EST 21-APR-1997
EST89818 Small intestine II Homo sapiens cDNA 3' end, mRNA
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AA377278.1 GI:2029596
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AUTHORS
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Search completed: September 18, 1999, 06:47:49 Job time: 3666 sec

Perfect score: Sequence: Scoring table:

Searched: Database

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Run on:

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AC006804 Caenorhab AC006842 Caenorhab AC006842 Caenorhab AC006840 Caenorhab AC006840 Caenorhab AC006447 Mus muscu AL022105 Human DNA M132.2 Chicken Car L31504 Neurospora AC003029 Homo sapi AC030476 Carcine Car L31504 Neurospora AC001657 Drosophil AC021933 Mycobsphil AC021933 Mycobsphil AC030476 Gazella SAF030476 Gazella SAF030476 Gazella SAF030481 Gazella SAF030481 Gazella SAF030481 Gazella GAF030485 Gazella GAF030485 Gazella GAF030486 Gazella GAF0304866 GAF030486 GAF0304866 GAF030486 
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ACO06466 Homo sapi
ALO34390 Leishmani
ACO07778 Homo sapi
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297209 S.pombe chr
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D49396 Human mRNA
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Kornman, K.S. and Duff, G.W.
Detecting genetic predisposition to
Patent: US 5686246-A 1 11-NOV-1997,
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HS2C002115
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AC003029
HS85661
AC004340
AC001657
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MTV038
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Sequence 1 from patent US 5686246.
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                                                                                                                                      9; Search time 436.05 Seconds (without alignments)
196.923 Million cell updates/sec
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                    GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                         679419 segs, 1590154680 residues
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27
1 AAGCTIGTTCTACCACCIGAACTAGGC
                                                                                                                                      September 18, 1999, 15:49:29
                                                                                                   - nucleic search, using sw model
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23-DEC-1997

Score

Result No.

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HTG: HTGS_PHASE1.
Caenorhabd:i.1s elegans.
Caenorhabd.is elegans.
Eukaryota: Metazoa: Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
I (bases 1 to 145614)
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Caenorhabditis elegans clone Y53G8B, WORKING DRAFT SEQUENCE, i
unordered pieces.
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ON Mar 1, 1999 this sequence version replaced gi:4263134.
* NOTE: This is a "vorking draft" sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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11863. .11970
/note="Alu repetitive sequence"
a 2489 c 2226 g 3547 t
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/note="poly[dA-dC] tract"
8912. 9137
/note="5 x 46 bp repeat"
9770. 9806
/note="poly [dT-dG] tract"
10290. 11643
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7695. .7744
/note="poly [dA-dC] tract"
7815. .7939
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Waterston, R.H.
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                    /number=3
3215. .4102
/number=3
4103. .4325
/number=4
4326. .6261
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/note="Alu re
6262. .6432
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Best Local Similarity 100.
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/translation="MAKVPDMFEDLKNCYSENEEDSSSIDHLSLNQKSFYHVSYGPLH
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DSEEIIKPRSSPFSFLSNWKYNFMFIRYEFILNDALNQSIIRANDQYLTAAALHNL
DBAVKFDMGAAYKSSKDDAKITVILRISKTQLYYTAQDEDQPVLLKEMPEIPKTITGSE
TNLLFFWETHGTKNYFTSVAHPNLFIATKQDYWVCLAGGPPSITDFQILENQA"
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Prinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 11970)
Furutani,Y., Notake,M., Fukui,T., Ohue,M., Nomura,H., Yamada,M. and
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1375. 1382
/note="direct repeat 1"
1375. 1390
/note="pot. transcription activator (seq. homolog. to adenovirus 2 major late promoter transcription factor
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   Gaps
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Location/Qualifiers
1. 11970
   Indels
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Human gene for interleukin 1 alpha (IL-1 alpha).
X03833
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1375. .1382
1383. .1390
/note="inverted repeat A"
1383. .1390
/note="inverted repeat A'"
/note="direct repeat A'"
/note="direct repeat I"
   Mismatches
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/db_xref="taxon:9606"
254. 393
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/db_xref="PID:933786"
/db_xref="GI:33786"
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
1 (bases 1 to 145614)
Waterston,R.H.
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Submitted (24-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Loui
Mo 63108, USA
MO 63108, USA
ON Mar 1, 1999 this sequence version replaced gi:4263476.
* NOTE: This is a "working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Caenorhabditis elegans clone Y53G8Y, WORKING DRAFT SEQUENCE, E
UNDOCACE PROCES.
runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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19071: gap of unknown length
27630: contig of 8559 bp in length
27639: gap of unknown length
54395: contig of 26756 bp in length
54404: gap of unknown length
564123: gap of unknown length
56423: gap of unknown length
145614: contig of 89191 bp in length.
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/db_xref="taxon:6239"
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84.0%; Pred. No. 79;
tive 0; Mismatches
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Waterston, R.H.
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditina; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis:
Materston, R.H.
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Caenorhabditis elegans clone Y55D5, WORKING DRAFT SEQUENCE, 4
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Submitted (24-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="Y53G8Y"
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84.0%; Pred. No. 79;
live 0; Mismatches
                                                                                                                                                                   68.9%; Score 18.6; D
84.0%; Pred. No. 79;
iive 0; Mismatches
                                                                       25159 g 47086
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HTG; HTGS_PHASE1.
                                                                       25460 c
                                                                                                                                                                                                                    21; Conservative
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Best Local Similarity
Matches 21; Conserv
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="p22.1-22.3"
/clone_lib="RPCI3"
444. .516
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/gene-"dJ501N12.1"
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                           (bases 1 to 170952)
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/note="L1 rep
4030. .4359
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                                                                                                                                                                                                                                                                                                   The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens DNA sequence from clone 501M12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another anknown gene. Contains ESTs, STSs and GSSs, complete sequence.
                       ACO06447 151528 bp DNA HTG 09-JUN-1999
Mus musculus, WORKING DRAFT SEQUENCE, 5 unordered pieces.
AC006447
                                                                                                                                                                                              Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                              On Jun 9, 1999 this sequence version replaced gi.4580404.

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                    Mus musculus
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; I. (bases 1 to 151528)
Wu,H., Yao,Z., McDermid,H. and Roe,B.A.
Mus musculus Chromosome 6 BAC Clone 67d14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5480: contig of 5480 bp in length 5555: gap of unknown length 12748: contig of 7193 bp in length 12823: gap of unknown length 37024: contig of 24201 bp in length 82029: contig of 44930 bp in length 82029: contig of 44930 bp in length 82104: gap of unknown length 82104: gap of unknown length 151528: contig of 69424 bp in length
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84.0%; Pred. No. 79;
Live 0; Mismatches
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/db_xref="taxon:10090"
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82104:
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12748:
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ORIGIN
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AUTHORS
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RESULT
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KEYWORDS
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Direct Submission

Submitted (06-JUL-1998) E-mail enquires: humquery@sanger.ac.uk

Clone requests: clonerequest@sanger.ac.uk

On Jul 1, 1998 this sequence version replaced gi:2980811.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

only a small overlap as described above. This sequence submission

only a small overlap as described above. This sequence is the

entire insert of clone 501N12. This sequence has been finished

according to sequence map criteria as follows. An attempt is made

to resolve all sequencing problems, such as compressions and

repeats, but not necessarily within known annotated human repeat

sequence elements (e.g. Alu). Where the sequence is ambiguous,

there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of

human chromosome 6 mapping group and Armin Volz & Andreas Ziegler.

Puther information and attempt attempt and armin volz & Futher Puther information and attempt and armin volz & Futher Puther Arman Volz & Andreas Ziegler.
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AIQEDLKSAERLMRDAKNSKTLLPNLYHVGGASWAGASGLLSSPIQETLESMAGEVTR
VVDEQLKALLESMVDAAENLCPNVMKKAHIRQDLIHASTEKISIPRTFVKNVLLEQSG
IDILNKISEVKLIVASFLSDRIVDEILDALSHCHHKLADHFSRRGKTLPQQESLEIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/HGP/Chr6/ 501N12 is from the library RPC13 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2. Location/Qualifiers 1.170952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7659. .7776
/note="AluYb8 repeat: matches 191. .308 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 1432. .1968 of consensus"
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/note="AluJb repeat: matches 280. .1 of consensus"
complement(1341. .1477)
/note="MIR repeat: matches 237. .85 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Alux repeat: matches 1. .296 of consensus" complement(4554. .4853)
/note="AluJo repeat: matches 301. .1 of consensus" 6829. .34852
/gene="dd501N12.1"
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/note="AluSg repeat: matches 1. .239 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: cDNAs Y10518 Y10519 Z83950 Y10508"
/codon_start=2
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32011. .32098,34703. .>34852)
/gene≂"dJ501N12.1"
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7659. 7776
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/protein_id="CAA18156.1"
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/db_xref="PID:9335565"
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/db_xref="SPTREMBL:075660"
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/ Jacobs. 12048
// Action 100 | Conserved | Complement (22914. 23103)
// Action 100 | Complement (2300 | Consensus | 24701. 2489
// Action 100 | Complement (2300 | Consensus | Complement (2300 | Consensus | Complement (2300 | Consensus | Complement (27877. 28054)
// Action 100 | Consensus | Complement (27877. 28054)
// Action 100 | Consensus | Complement (27877. 28054)
// Action 100 | Consensus | Complement (2812. 2868)
// Action 100 | Consensus | Complement (2812. 2868)
// Action 100 | Consensus | Complement (3812. 2868)
// Action 100 | Consensus | Complement (3810. 3809)
// Action 100 | Consensus | Complement (3810. 3809)
// Action 100 | Consensus | Complement (40249. 40548)
// Action 100 | Consensus | Complement (40249. 40548)
// Action 100 | Consensus | Complement (40249. 40548)
// Action 100 | Consensus | Complement (40249. 40548)
// Action 100 | Consensus | Complement Action 100 | Consensus | 
                                                                                                                                /note="Aluxx repeat: matches 273. .1 of consensus" complement(10099. .1022)
/note="Aluxp repeat: matches 303. .179 of consensus" 11294 .11503
/note="MIR repeat: matches 4. .214 of consensus" complement(12237. .12525)
/gene="dJ501N12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER21B repeat: matches 790. .703 of consensus complement(16545. .16637)
/note="MER39 repeat: matches 676. .582 of consensus" complement(16603. .17427)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MERRIE repeat: matches 792. .4 of consensus" 17480. .17647
/note="AluSp repeat: matches 136. .303 of consensus" complement(19382. .19433)
/note="LiHS repeat: matches 578. .526 of consensus" complement(19656. .19960)
226099 .22648
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/note="MIR2 repeat: matches 30. .134 of consensus" complement(45009, 45166)
/note="MIR repeat: matches 180. .21 of consensus" complement(47974. .48264)
/note="Ally repeat: matches 301. .2 of consensus" complement(48410. .49073)
/gene="d5501N12.2"
/note="And repeat: matches 301. .2 of consensus" complement(48410. .49073)
/gene="d5501N12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR2 repeat: matches 146. .28 of 1448. .15519
/note="MIR2 repeat: matches 74. .145 of complement(15866. .1633)
/gene="ASGAN12.1"
/note="match: GSS A0016561"
complement(16512. .16606)
                                                                                                                                                                                                                                                                                                                                                                                /note="match: EST AA639318" complement(12599. .12717)
                                                                    /note-"match: GSS B37778
complement(8536. .8952)
/gene="dJ501N12.1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases Ito 103574)

Lamerdin,J.E., McCready,P.M., Adamson,A.W., Burkhart-Schultz,K., Garcia,E., Kyle,A., Ramirez,M., Stilwagen,S., Garnes,J., Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D., Kobayashi,A., Olsen,A.O. and Carrano,A.V.

Sequence and Carrano,A.V.

1 (unpublished (1997)

2 (bases 1 to 103574)
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/evidence=not_experimental
                                                                                     HSACO02115 103574 bp DNA PRI 30-JUN-1997 Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete
                                              /note="MEM2" repeat: matches 348. .1536 of consensus"
50415. .50724
                                                                                                                                                                                                                                                                                                                                                                                                                                                     63567. .65020

/note="SVA repeat: matches 4. .1372 of consensus"
complement(65545. .65881)
/note="match: STS G05436"
complement(6517. .66232)
/note="MER2 repeat: matches 345. .9 of consensus"
complement(67491. .67789)
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complement(68357. .68845)
/note="Aluyb repeat: matches 3768. .3579 of consensus"
/note="L1 repeat: matches 3768. .3579 of consensus"
                                                                                                                                                                                                                                                                                                                                                         /note="MidO repeat: matches 301. .6 of consensus" 62452. .6.2015
/note="MER34 repeat: matches 48. .409 of consensus" 62854. .62898
/note="MER34 repeat: matches 480. .525 of consensus"
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95.0%; Pred. No. 98;
iive 0; Mismatches
complement(48410, .49073)
/gene="dJ501N12.2"
49166. .50348
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/gene="dJ501N12.3"
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ACO02115.1 GI:2098573
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/rpt_family="ALU"
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3429. 3705
/rpt_family="ALU"
3429. 3705
/rpt_family=ALU"
3755. 4205
/rpt_family=ALU"
3755. 4205
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score: 5.76=29; database searched: nr; hypothetical L1
protein (third intron of gene TS)- human >prf||1510254A L1
repetitive element ORF [Homo sapiens]"
/rpt_family="L1"
/rpt_family="ALU"
/rpt_family="ALU"
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                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (13-MAY-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
R31396 from 1- 36,162; F2S451 from 25,661-55,793; R31076 from
66,237- 103,574.
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rame: 0, quality: excellent, score: 94.000"
0193. .10276
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                                                                                                                                                                              1. .103574
/organism="Homo sapiens"
/db_xref="Lexon:9606"
/clone="R31396-F25451-R31076"
/chromosome="19"
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/rpt_family="ALU"

11801. .12092

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complement(12570. .12861)

/rpt_family="ALU"

12958. .13233
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/rpt_family="ALU"
complement (4822. .4931)
/rpt_family="MIR"
5127. .5417
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complement(7534. .7834)
/rpt_family="ALU"
complement(8629. .8915)
corp. complement(8629. .8915)
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/rpt_family="L1"
complement(2199.
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22690. .22803
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700te="predicted exon, program: grail2exons_human_1.3,
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23377. .23497
70ote="predicted exon, program: grail2exons_human_1.3,
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14234. .14310
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complement(20717. .20970)
.iote="predicted exon, program: grail2exons_human_1.3,
.iote="predicted exon, program: grail2exons_human_1.3,
.21268. .21858
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complement(19351. .19626)
/rpt_family="ALU"
19697. .19833
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5516
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complement(28025. .28395)
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24305. 24583"MFR21"
/rpt_family="ALU"
25093. 25377
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conplement (2589). 2
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complement(15950.
/rpt_family="ALU"
16665. .17493
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14946 . 15122
/rpt_family="L1"
1797 . 15445
/rpt_family="ALU"
15584 . 15619
                                                                                                                                                                                                                                                                                                      rpt_family="ALU" 7507.
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complement(18269.
                                                                                                                                                                                                                                                                                                                                                                                                     pt_family="ALU"
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20425. .20701
                                                                                                                                                                                                          .5584. .15619
/rpt_family="ALU"
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27474. .27765
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21922. .22503
                                                                                                                                                                                                                                            complement (15626
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ACCESSION
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/protein_id="AAA48940.1"
/protein_id="AAA48940.1"
/db_xref="91:212260"
/db_xref="G1:212260"
/translation="MTSLLFLVLISVCWAEPHPDNSSLEHERIIHIQEENGPRLLVVA
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Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Archosauria;
Aves: Neognathae: Galliformes: Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 1910)
Deak,F., Kiss,I., Sparks,K.J., Argraves,W.S., Hampikian,G. and Goetinck,P.F.
                              complement(29166. .29667)
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complement(29979. .30276)
/rpt_family="ALU"
30918. .31090
/note="predicted exon, program: grail2exons_human_1.3, frame: 1, quality: excellent, score: 95.000"
                                                                                                                                                                                                     /rpt_family="ALU"
complement(31848...19968)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: marginal, score: 45.000"
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/note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: excellent, score: 94.000"
complement(32823...33089)
33296...33518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="predicted exon, program: grail2exons_human_1.3,
rame: 1, quality: excellent, score: 97.000"
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Proc. Natl. Acad. Sci. U.S.A. 83, 3766-3770 (1986)
86233315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHKLNKPA 1910 bp mRNA VRT
Chicken cartilage link protein mRNA, complete cds
M13112
9212259
M13212.1 GI:212259
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Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. 1910
/organism="Gallus gallus"
/db_xref="taxon:9031"
136. .1203
/rpt_family="THE1"
complement(28597. .28876)
/rpt_family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .34170)
                                                                                                                                                                                                                                                                                                                                                                      33296 . .33518

/rpt_family"MER1"

3532 . .3829

/rpt_family"ALU"

33885 . .33983

.7rpt_family"MER1"

complement(34062. .34170

/note="predicted exon, pr
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/rpt_family="ALU"
35483. .35637
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87.0%;
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Matches 20; Conservative
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KEYWORDS
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ORGANISM
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Draft entry and computer-readable sequence for [1] kindly submitted by I.Kiss, 04-JUN-1990.

Location/Qualifiers

1. 460
EQAKIFSQRGGNVTLPCKFYHEHTSTAGSGTHKIRVKWTKLTSDYLKEVDVFYAMGHH
KSYGKYGGRYCLRESSENDASLITHUMLEDYGRYKCEVELBELEDDYAVVALULEGV
VFPYSPRLGYRVLNFFEAOOACLDODSIIASFDOLYZBAWSGLDWCRAGWLSGSVQY
PITKPREPCGGKNTVPGVRNYGFWDKERSYRVDVFCFTSNFNGRFYYLIHPTKLTYDEA
VQACLKAGAQIAKVGGIFAAWKLLGYDRCDAGWLADGSVRYPISRPRKRCSPNEAAVR
389 C 408 9 519 t
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cartllage link protein.
2 of 5
Chick (domesticus, strain White Leghorn) 9-day embryo DNA, clones lambda gLP39.13 and lambda gLP33.7.
Gailus gallus
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Kiss,I., Deak,F., Mestric,S., Dellus,H., Soos,J., Dekany,K., Argraves, Y.S., Sparks,K.J. and Goetinck,P. Structure of the chicken link protein gene: Exons correlate with the protein domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEUROIDHC 14313 bp DNA PLN 07-APR-1995
Neurospora crassa cytoplasmic dynein heavy chain (ro-1) gene,
complete cds.
L31504
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/db_xref="taxon:9031"
<1. .>460
/note="cartilage link protein mRNA and introns"
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0
                                                                                                                                                                                         66.7%; Score 18; DB 4; Length 1910;
80.8%; Pred. No. 1.6e+02;
Live 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 84, 6399-6403 (1987)
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/note="cartilage link protein intron C"
90 c 113 g 112 t
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/note="cartilage link protein intron
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Chicken cartilage link protein gene, exon 3.
M35036
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/number=3
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Matches 2
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DEFINITION
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ORIGIN
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ORIGIN
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KEYWORDS VERSION

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FKPTFNPNTPLGQTGSKVSETKHVMF1REFAASVSLLQSKTLLLANIYVTVQKALNEL
KTCPFRASAROSRLETIQHAVDQLNLEDZYNLGSVWERWNROKTKDULYTYTLQVALQAW
IQAFEDEDVERPSERKILLETAXDBAKSIGPVIKSLVHETTMRNQYIYLDPPLEYAR
ASWFAQLQDWIGVICNLKKIKATRYTMSLSTEVVDEPRFNDLPGDCTEELLRVQTSVE
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RSFGHITIDYDQVQTKVNAKYDQWQQDILIKFASRLGNRMREVYAELEKARKDLEGQA
MTANSTAEAVRFITIVQSCTRQVKLWAPEIETFRQGESTLVRQRYHFQNDWLHAEQVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="cytoplasmic dynein heavy chain"
/protein_id="AAA64908_1"
/protein_id="Plote 1908_1"
/db_xref="Eli:473490"
/db_xref="GI:473490"
/translation="MMDSVPSPPPQPSPDANGVATTPFAAVDPVKVVDHLVLLEATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDQYMKKVEQVLGSDWALHTEGGKLQNESDLFRKKLDTRPIFEAWLHDVQRKQISISG
LLFTINRIRSAGNILELAVNFDAQVIALFKETRNLLMLNYPVPHSVNNVAKEAKRYYP
FAVSLMESVRIFAQTNRQISDMSEVAVLLSGHRNDVYTLISKGIPLRWETFVNTYEVH
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DVASATLTHFEQRITKLQEESAMVAKAKEALDLAPTPDTSLGVILEEVQDFKSVWASL
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HSPYYKEFEEEASSWEEKLNRVHVLFDIWIDVQRQWYYLEGVFHGNADIKHLLPIESS
RFQNINSEFLAVMKKVYKQPNVLDVLNIPNYQKSLERLAELLNKIQKALGEYLEKERV
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MNTYPSQIVVLATGVVWTTAVDQALADGGKDLQLLFDREVQVLRMLADTVLGDLEVLL
RKKCEQLITECVHQRDVIEKLVKLNANSNTHYMWLLQMRYVYNPEGDFLQRLHIKMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAKRDELEAPGSLLSKVRYSDTVQRCSRFALDTQVALYIQKDLAPTTTLDGDNGAEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPEPTHVYTISSDLTSSPTTVAYLVLLKRPQPLDPIVPLTSQIQMLNLPGPAYLSTSG
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ELELSLSHLQQNVEIPEVSLPFHPLVQSTLEEAATKNVKPSIDLLPATVLADSTFLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQATVNNWIKSIQVITKMTRDPTTGTANQEINFWLSMEAALEGIENQLRSEGVMLTLD
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FGHLNKKLRICPYPIRRALPLVEAISGDLDEVLHRLLPGTELVKLDYEEFKGVMKQAG
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RTIINVLGPKATVNGIVTASGANGVAVVEEIGDVDAVDEVKQAWEALKDVDLLDCTRE
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KVNSILGELKSEAVRDRHWTKIYKQIKPGKRYSPVSMTLGDVWDLNLVATEVIVKDII
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KYVPASLEKLOEAIRRLAAERQLVVNDIWMTKVLOLYQIQKIHHGVMMYGNSGSGKSA
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GTSSLIDFTVTMPQGEWQTWQQHVPTIEVNTHSVTQTDVVI PTLDTIRHEDVLYSWLA
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                                                                                                                                                                                               Sordariales; Sordariaceae; Neurospora.
I (bases 1 to 14313)
Plamann.M., Mike,P.F., Tinsley,J.H. and Bruno,K.S.
Cytoplasmic dynein and actin-related protein Arpl are required for normal nuclear distribution in filamentous fungi
J. Cell Biol. 127 (1), 139-149 (1994)
                                                                                                                                                               Euascomycetes; Pyrenomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .14313
/organism="Neurospora crassa"
/b_xref="taxon:5141"
join(173. .482,549. .12853,12926. .13414)
/gene="ro-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(173. .482,549. .12853,12926./gene="ro-1"
                                        cytoplasmic dynein heavy chain
                                                                                                                  Neurospora crassa
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                             Neurospora crassa DNA.
L31504.1 GI:473489
                                                                             SOURCE
ORGANISM
                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
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MEDLINE
FEATURES
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ELTHSVÜLDRPWITAPDTTEVATRGLINLPPEHREAVVNAMVTITISCHRAKLLKOO
GKITFLTPRHELDFVAQVVLXURKREDLEEGORHLWGLEKLRDTUDKVRDLRYTLS
ERKÄQLEGORALEDFVAGEARASVESTRRULTLES
LARAEPAVEEAARASVESTRRULTEVRSMPTPPSGVKLALESVCTLIGHRANDMKTIG
GIVRRDDFIASIVNENNEKQMIKSLRVKRNREFETANPEFFTERVVRASRACGPLVOWV
EAQVNYABILLDRVGPLREEVMLEEGOALQTRAEARAVEQTISTLENSIARYTETAAAL
SETOAIKAEMSRVOFKVORSVKLLDSLSSERTRWEGSRSFETOISTLENSIARYTETAAAL
SETOAIKAEMSRVOFKVORSVKLLDSLSSERTRWEGSRSFETOISTLENSIARYTETAA
FLAYSGLYDQTRKSMMEDMHQLHLSGVOFKQHNPMTEYLSTADERLSWQENTLEVD
DLCTENAILLKRFNRYPLIIDPSGRAFEFLNRESKREKLYSTADERLSWGENTLEVD
FGNPILLQDAEHLDPVAHYLNKEYOKTGRYLIOGGKQUDFSPARKLYLSTREPSA
TFAPDICSRTTYNFTYTOSSLQTOSLNEVLKSERPDVDERRSNLIKLGFFFVHLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                    LEKKLLQALNESRGNILDDDHVIETLETLKTEAAEISAKMSNTEGVMAEVEOITLOYN
IIARSCSAVFAVLEQLHYLNHFYRFSLQYFLDIFHSVLRGNPHLANETNHNVRRDIIV
KDLFVATFKRTALGLLQKDRITLAMLLAQASPYKMDKGLLDIILDERIEGKDVSIDQN
LSKNYVPVDREQLRDFVKARLKTFCEEEVDVPLILENDVLEHVLRIDRVFROPOGHLI
IGYVSGSKTTLSRPVAMMGLKVPOIKVHGKYSAEDFDEDLREVLRFGCKGFKICF
IMDESNYLDSGFLERMNTLANAEVPGLFEGDDLAALMTACKEGAGRGGLLLDSOEEL
YKWFTGOIVKNLHVPFTMNPGEDGLSSKAATSPALFNRCVLNWFGDWSDQALFOVAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TREEAFARAKKIPALKNKIDAVPEADWEKFFTEELAEDFVPKIWNDETEPNDRALMSL
LLVKLFRLDRFVPAAERFVTLVFGSDLFDIVEDLKQTVDQVSAILPIALVSSPGFDAS
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KKMETLNPNPEFRLFLSMESSPKIPVNLLRASRVLMYEQPAGVRANMKDSMSSISTRS
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EVSHDAEDEOKDAATGGDLVVPSGTSLOEFMSWIQKLPEREPPTYLGLPANAEKLLLV
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80.8%; Pred. No. 1.5e+02;
V.cmatrhes 5; Indels
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9077. .10000
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549. .12853
/gene="ro-1"
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/gene="ro-1"
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Best Local Similarity
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12241. .12529
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complement(12530. .12557)
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12631. .12765
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complement(9788. .10134)
/rpt_family="THE1B"
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/rpt_family="LIME1"
10201. .1049?
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complement(2374. 2612)
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complement(2631. 2799)
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complement (3608. 4064)
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complement (4099. 4364)
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complement (4374. 4672)
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6185. .6402
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complement(7325. .7487)
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                                          /rpt_family="FRAM"
complement(2260, .2370)
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4761, 4893
                                                                                                                                                                                                                        complement(2800. 3099)
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complement(7947. .8248)
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complement(9202. .9433)
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5403. .5684
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2100. .12229
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/rpt_family="Alusx"
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complement(2001. .
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/note="Overlaps with bases 1-226 in AC002996."
/note="Region: Overlap with AC002996"
/join(88. .201.843. .945,1380. .1564,6860. .7024,8688. .8845,
12641. .12755,18325. .18759)
/gene="Human nucleus-encoded mitochondrial aldehyde
                                                                                                                        Muzny, D., Arenson, A.D., Adams, C., Bunac, C., Carvelli, K., Chang, J., Chacko, J., Chen, J., Ding, Y., Dugan, S., Durbin, J., Forcum, J., Gancia, C., Goodman, M., Gorrell, J. H., Harwood, M., Hernandez, J., Jackson, L., Jin, S., Kampal, R., Karpathy, S., Kovar, C. Lau, S., Leal, B., Lee, E., Li, Y., Lichtarge, O., Liu, M., Logan, O., Lu, J., Ly, T., Marondel, I., Martinez, C., Merscher, S., Montgomery, K., Scherer, S.E., Shen, H., Simon, M., Stovall, K., Timms, K.M., Todd, J., Nelson, D. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 31, 1998 this sequence version replaced gi:2909690. Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (31-JUL-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 139166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases I to 139166) Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence similarities were identified using Powerblast by Jinghui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The repeat regions shown were identified using RepeatMasker by
                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (27-oCT-1997) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
(bases 1 to 139166)
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 139166)
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/note="Unigene cluster Hs.74630, K03001, X05409"
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/db_xref="taxon:9606"
/clone="RPC13-462E2"
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/rpt_family="AluJb"
                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 139166)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                              Homo sapiens
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9433)

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Diosophila melanogaster

Eukaryota Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Medezoa, Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Meoptera; Endopteryota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

CE 1 (basea 1 to 51009)

RS Celniker; S.E., George, R.A., Galle, R.F., Hoskins, R.A.,

Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E.,

Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,

Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S.,

Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,

Pfeiffer, B., Punch, E., Taveney, B., Wan, K.H., Whitelaw, K.R.,

Yee, A., Zhang, R., Zieran, L.L. and Kimmel, B.

Sequencing of Drosophila chromosome, region 22E1-22E1

Unpublished (1997)

CE 2 (bases 1 to 51050)

RS Celniker; S.E., George, R.A., Galle, R., Svirskas, R.R., Hoskins, R.A.,

Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chavez, C.,

Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A.,

Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E.,

Shir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R.,

Zieran, L.L. and Kimmel, B.E.

Direct Submission

Albmitted (07-MAR-1998) Drosophila Genome Center, Lawrence Berkeley
              L SUBMITTED (1997-MAY-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquires:

Cambridgeshire, CB10 15A, UK. E-mail enquires:

Numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Mar 22, 1999 this sequence version replaced gi:4376009.

IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known: 800 n's separate segments. Unfinished: dJ856G1 Contig_ID: 01260 acc-AL03381

Length: 151795 bp.

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Drosophila melanogaster DNA sequence (Pl DS07020 (D238)), complete
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Pred. No. 1.5e+02;
0; Mismatches 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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80.8%;
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Best Local Similarity
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AC004340
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/standard_name="DWC10/DWC11"
/note="GDB:179565, Chr. 12q24.2-1~2q24.2, Homo Sapiens"
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Homo sapiens chromosome 6 clone 856G1, WORKING DRAFT SEQUENCE,
unordered pieces.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 151795)
Phillips,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="AluJo"
18511. .18642
/gene="Human nucleus-encoded mitochondrial aldehyde
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Pred. No. 1.5e+02;
0; Mismatches 5;
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complement(19388. 19650)
/rpt_family="AluJo"
19837. 2015:
                                                                                                                                                                                                                                                                                                                                                                                                         complement(16333. .16541)
/rpt_family="L2"
complement(1658. .16956)
/rpt_family="AluSx"
16992. .17186
17092. .17186
1705. .17506
                                                                                                                                         /rpt_family="AluJo"
complement(14148. .14404)
/rpt_family="AluJb"
14525. .14811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluSp"
complement(20254. 20555)
/rpt_family="AluSx"
complement(20559. 21050)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="Alusx"
complement(17550. .17928)
/rpt_family="L2"
17954. .18213
                                                        /rpt_family="Alusx"
complement(13595, .13622)
/rpt_family="AT_rich"
13999, .14103
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/db_xref="dbSTS:17970"
18807. .19105
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15767. .16064
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|4814. .15118
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15472. .15768
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HTG; HTGS_PHASE1.
                                          13248. .13548
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Best Local Similarity 80.8%;
Matches 21; Conservative
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NESCONDERS: E., George, R.A., Galle, R.F., Hoskins, R.A.,

RS Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A.,

Syirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E.,

Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E.,

Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S.,

Noshrefi, A.R., Noshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,

Ffeiffer, B., Punch, E., Sair, E., Twomey, B., Wan, K.H., Whitelaw, K.R.,

Yee, A., Zhang, R., Zieran, L.L. and Kimmel, B.

Sequencing of Alcohol dehydrogenase region

AL Unpublished (1997)

SR Martin, C.H., Arcaina, T.T., Bondoc, M.M., Chiang, A., Critz, P.A.,

Bavis, C.A., Doyle, C.M., Ericsson, C.L., Farfan, D.E., Gunning, K.M.,

Houston, K.A., Jaklevic, M.A., Kadner, K.E., Kim, K., Kim, S.F.,

Ko, C.L., Lewis, K.D., Li, M., Lindquist, K.J., Lomotan, M.A.,

Lustre, V.M., Machula, M.U., Mayeda, C. R., Miguel, T.M., Miller, C.A.,

Man, K.H., Whitelaw, K.R., Yee, A., Yeh, R.T., Yu, C. and Palazzolo, M.J.,

Direct Suhmission
Laboratory, MS 64-121, Berkeley, CA 94720, USA on Jul 7, 1998 this sequence version replaced gi:3228456. Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send email to drosophila@mhgc.lbl.gov.
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Drosophila melanogaster DNA sequence (Pl DS06874 (D19)), complete
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Ac001057.136286 L36305 L36304 L36289 L36300 L39666 L36301 L36298
Ac001057.136286 L36280 L36670 L39668 L36284 L36285 L36295 L39667
L36296 L36287 L36299 L36291 L36297 L36284 L39671 L39665 L39669
L36229 L36293 L36302 L36290
AC001657.1 GI:2337899
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On Aug 20, 1997 this sequence version replaced gi:1945585.
Sequence submitted by:
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80.8%; Pred. No. 1.5e+02;
Live 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                             /organism*"Drosophila melanogaster"
/db_xref="taxon:7227"
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11189 c 11359 g 14134 t
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 18, 1999, 05:27:26 ; Search time 213.04 Seconds (without alignments) 31.709 Million cell updates/sec Run on:

US-09-037-472-9 27 Title: Perfect score: Sequence:

1 AAGCTTGTTCTACCACCTGAACTAGGC 27

IDENTITY\_NUC Scoring table: 311585 seqs, 125096042 residues Searched:

N\_Geneseq\_36:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	,,,	* Query				
No.	Score	Match	Match Length DB	60	QI	Description
П	27	100.0	27		V32389	Interleukin-1-
. 4	22	81.5	22		T70316	Primer for det
(*)	3 22	81.5	5701	Н	X02988	Human IL-1ra B
4	1 21	77.8	21	Н	X16611	Interleukin 1
u)	5 18	66.7	327	П	V78683	Staphylococcus
U	17.4	64.4	633	-	V75647	Staphylococcus
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ω	3 17.2	63.7	648	П	686LA	Staphylococcus
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c 12	16.6	61.5	7753	-	026727	Encodes exons
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6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

X20559 Polynucleotide seq X30293 Borrelia burgdorfe	ALIGNMENTS	-945). CR; primer; amplifica thy; interleukin-1-al ; SS.	reducting increased risk of signt-treatening diabetic retinopathy comprises identifying genetic polymorphism pattern for genes II-1A, IL-1B and IL-1RN, useful to allow treatment before clinical symptoms occur.  Claim 2; Page 33, 41pp; English.  Interleukin-1-alpha (IL-1-alpha) primers 1 and 2 (V32390) were used to amplify the IL-1-alpha gene region to identify single base variation polymorphism of C/T at base 889. The invention claims to provide a method for predicting the risk of sight threatening diabetic retinopathy. The method involves isolating DNA from a patient and determining the polymorphism pattern of the genes that code for interleukin-1-alpha, interleukin-1-beta and interleukin-1RN. The polymorphic pattern interleukin-1-beta and interleukin-1RN. The polymorphic pattern determination of the genes that carrying a genetic polymorphism patterns thereby identifying patients carrying a genetic polymorphism associated with increased risk of sight threatening diabetic retinopathy. The method may be able to identify diabetic patients at risk before the clinically detectable disorders occur. Polymorphism pattern determination of IL genes involved PCR reactions using primers V32389. The method is also claimed to be useful in conjunction with identification of other genes associated with sight threatening diabetic retinopathy in genomic DNA and therefore, in identifying diabetic patients expressing multiple risk patterns.	Score 27: DB 1; Length 27; Pred. No. 0.00056; 0; Mismatches 0; Indels 0; Gaps 0; AGGC 27
0 5504 1 0 73 1		189 standard; DNA; 27 BP. 89; BP; BP; BP; BP; BP; BP; BP; BP; BP; BP	recurring increased risk of sign comprises identifying genetic Symptoms occur.  [L-1A, IL-1B and IL-1RN, useful symptoms occur.  Interleukin-1-alpha (IL-1-alpha) amplify the IL-1-alpha gene regingly the IL-1-alpha gene regingly the IL-1-alpha gene reging for predicting the risk of The method involves isolating DN polymorphism pattern of the gene interleukin-1-beta and interleuk identified is then compared with patterns thereby identifying pat associated with increased risk of the method may be able to identified in the method may be able to identificating the method is alberto identification of IL genes involv v32398. The method is alberto claimidentification of other genes as retinopathy in genomic DNA and the patients expressing multiple risk Sequence 27 BP; 7 A; 8 C	tch  27; Conservative 0; M  27; Conservative 0; M  AAGCTTGTTCTACCACCTGAACTAGGC
2 60. 2 60.		standard; Di 1998 (firs: 18th-1-alpha 18th-1-alpha; geneti; 18th-1-beta 18th-1-beta 18th-1-beta 18th-1-beta 1897; G0279, 1997; G0279, 1997; GB-02, 1997; GB-02, 1	rises ident Tib. 1B and Tib. 1	Similar 7; con CTTGTTC [
16. 16.		V32389; V32389; V32389; V32389; V32389; V32389; V32389; V32389; V32389; V3289; V3289; V3290; V320; V32	recomprises recomp	Y Ma Loco 1 1 1 1 7031 7031 7031 7031 701 701 701 701 701 701 701 701 701 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid encoding the new human cytokine Tango-77 - New isolated nucleic acid encoding the new human cytokine Tango-77 - New isolated nucleic acid encoding the new human cytokine Tango-77 - Stample 5; Figure 3; 226pp; English.

X02956.X03048 and X22301-X22304 are overlapping BAC genomic sequences containing alternatively spliced forms of human IL-1ra. Such fragments are used in the method of the invention which describes the isolation of a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a member of the cytokine superfamily that is expected to inhibit inflammation by binding to the interleukin-1 receptor (IL-1R). It may also bind to a new receptor so could require other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic hard also be a second of a second of arthritis, possissis and inflammatory and also second remarkable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human LL-1ra National DNA sequence 33.

Human: LL-1ra: cytokine superfamily; inflammation; inhibition; interleavin-1 receptor; LL-1R; regulation; asthma; rheumatoid arthritis; interleavin-1 receptor; LL-1R; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                Tile of the patient's genetic polymorphism pattern - allows are described of increased periodontal disease severity prediction of increased periodontal disease severity are districted of increased periodontal disease severity prediction of increased periodontal disease severity as Page 25; 33pp. English.

Solve of the primers (170316 and 11388-88) can be used in a new method for identifying a genetic predisposition to periodontal disease by continent from a genetic predisposition to periodontal disease by completed with severe disease were identified as IL-1B.

Alleles associated with severe disease were identified as IL-1B.

Alleles associated with severe disease were identified as IL-1B.

Completed to restriction disease of the primers are used subjected to restriction disease of determine the polymorphism at IL-1A base -889 can be identified wing primers (770316 and TIS84) corresponding to bases -967 to -945 and -888 to -869, crespectively. An NCOL site is create; if C is available at -889,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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02-AUG-1998; US-091650.
04-AUG-1997; US-054646.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or its receptor complex.
                                      (KORN/) KORNMAN K S.
(MEDI-) MEDICAL SCI SYSTEMS INC.
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                                                                                                                                                                                                                                                                                                                                            respectively. An NCOL sich but not if T is present.
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Best Local Similarity 100.
Matches 22; Conservative
   U12455.
US-510696.
                                                                    Kornman KS;
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WO9906426-A1.
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DB 1; Length 5701;

Score 22;

81.5%;

Query Match

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COURT, DUFF G.

COURT, DUFF G.

CAMP, DUSP, COURT, C.

CAMP, DUSP, C.

CAMP, DUSP, C.

CAMP, DUSP, C.

CAMP, DUSP, C.

CAMP, DORONA, D.

BY 199-080084, O.

New method of determining a patient's susceptibility to inflammatory disorder. Dy deterting the presence of an IL-1 (44112332)

The activity of proteins produced by the IL-1 gene cluster

The activity of proteins produced by the IL-1 gene cluster

The activity of proteins produced by the IL-1 gene cluster

The activity of groteer. The method comprises the detection of an interleukin I (IL-1) (44112332) haplotype in a sample obtained from the patient, where its presence indicates susceptibility to an inflammatory disorder. Mi6607 to X16631 represent PCR primer used in the method for detecting the IL-1 (44112332) haplotype. The method provides kits for the early prediction of a patient's susceptibility to inflammatory disorders, including coronary artery disease, osteoporosis, nephropathy in diabetes mellitus, alopecia areata, Graves disease, systemic lupus erythamatosus, lichen sclerosis and ulcerative colitis. The detection of alsorders, comprising diabetic retinopathy, juvenile chronic arthritis, psoriasis, and insulin dependent diabetes. The identification of a disease. Sociated haplotype enables determination of which alleles are causative, and this information is useful in designing treatment using various agents that modulate the activity of proteins produced by the IL-1 gene cluster are associated with particular contains and insulin determining genetic susceptibility to according the pathology of these diseases. Therefore, the use of IL-1 gene cultification in determining gene therapy with a mollogy of these diseases. Therefore the use of IL-1 gene cultification in the pathology of these diseases. Therefore the use of IL-1 gene cultification in manning genetic susceptibility to an intendent.
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Interleukin 1 (44112332) haplotype PCR primer #5.
Interleukin 1; IL-1; haplotype; inflammatory disorder; alopecia areata; coronary artery disease; osteoporosis; nephropathy; diabetes mellitus; Graves disease; systemic lupus erythamatosus; lichen sclerosis; ulcerative colitis; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                X16611 standard; DNA; 21 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGTTCTACCACCTGAACTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 A;
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Best Local Similarity 100.
Matches 21; Conservative
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1998; G01481.
29-MAY-1997; GB-011040.
(CAMP/) CAMP N J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COXA/) COX A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
WO9854359-A1.
                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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V78683
ID V78
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Sequence
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V77989
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                                                                                                                                                                                                                                                                                      anti-S. aureus vaccines
Claim 1; Page 2938; 3271pp; English.
This sequence represents one of 5191 Staphylococcus aureus DNA sequences
of the invention. The DNA sequences are recorded on a computer readable
medium, preferably selected from a floppy or hard disk, random access
of the invention. The DNA sequences are recorded on a computer readable
medium, preferably selected from a floppy or hard disk, random access
of the invention. The DNA sequences are recorded on a computer readable
menory (RAM), read-only memory (ROM) or CD-ROM, Homology searches using
the S.aureus DNA sequences allows putative functions to be assigned so
that protein-encoding or regulatory regions of commercial, therapeutic or
that protein-encoding or regulatory regions of commercial, therapeutic or
industrial importance can be obtained. Specifically, sequences which are
likely to encode antigens have been identified and these polypeptides can
be used in a vaccine composition against S.aureus infection. The
solvepeptides can also be used in a kit for the immunodetection of
S.aureus in a sample. S.aureus is implicated in numerous human diseases,
including cellulitis, eyelid infections, food poisoning, osteomyelitis,
skin and surgical wound infections, scalded skin syndrome, toxic shock
syndrome, etc. Organisms transformed with the DNA sequences can be used
for recombinant production of the polypeptides. The new DNA sequences
can be traced any of the Saureus DNA sequences contained on the
computer readable medium.
Sequence 327 BP; 87 A; 75 G; 77 T;
           16-MAR-1999 (first entry)
Staphylococcus aureus contig SEQ ID #4372.
Computer readable medium: vaccine; S.aureus infection; immunodetection; cellulitis; eyelld infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus config SEQ ID #1336.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                        WPI; 97-374922/35.
Polynucleotide(s) and proteins derived from Staphylococcus aureus
stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
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                                                                                                                                                            07-JAN-1997; 100117.

05-JAN-1996; US-009861.

(HUMA-) HUMAN ESCONDES SCI INC.

Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 AGTITGCTCTACCAATIGAGCTAGGC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-S.aureus vaccines
Claim 1; Page 1924; 3271pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AGCTTGTTCTACCACCTGAACTAGGC 27
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80.8%;
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Matches 21; Conservative
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05-JAN-1996; US-009861.
                                                                                                                Staphylococcus aureus.
EP-786519-A2.
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30-JUL-1997.
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                                                                                                                                                                                                                                Rosen CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V75647;
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, collypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, skin and surgical wound infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating computer readable medium.
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The present sequence encodes nitrile hydratase subunit beta, a novel protein isolated from Bacillus smithii. The protein has hydration activity for converting acrylonitrile into acryloamide. It is useful for producing amide from nitrile by biological catalysis.
Sequence 687 BP; 212 A; 112 C; 173 G; 190 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-1998 (first entry)
Bacillus smithii nitrile hydratase subunit beta encoding DNA.
Nitrile hydratase subunit alpha; nitrile hydratase subunit beta;
acrylonitrile; acryloamide; biological catalysis; amide;
thermally stable protein; ds.
Bacillus smithii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= Nitrile_hydratase_subunit_beta
/note= "No stop codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 G;
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86.4%; Pred. No. 32;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 C;
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18-MAR-1996; 060732.
18-MAR-1996; JP-060732.
(SUMO ) SUMITOMO CHEM CO LTD.
WPI; 97-520742/48.
P-PSDB; W32621.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T92382 standard; DNA; 687 BP. T92382;
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Best Local Similarity 94.7
Matches 18; Conservative
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Best Local Similarity
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99-081273/07
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Claim 1; Page 2639-2640; 3271pp; English.

Cofficient of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can likely to encode antigens have been identified and these polypeptides can
                                                                                                                                                                                        the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a simplicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scaleded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences
                                   Staphylococcus aureus config SEQ ID #3678.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyalid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                               /note= "these bases represent a line of missing text in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (and their fragments) are useful as primers or probes for isolating nomologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                          WPI; 97-374922/35.
Polynucleotide(s) and proteins derived from Staphylococcus aureus
stored on computer readable medium and used in the production of
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Sequence of human leukocyte interferon (leIFN) gene.
Interferon; yeast expression vector; promoter; ss.
                                                                                                                                                                                                                                                                              05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Pred. No. 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 C;
                                                                                                                                Location/Qualifiers
121. .180
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N40312 standard; DNA; 1253 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.7%;
82.6%;
standard; DNA; 648 BP
                             16-MAR-1999 (first entry)
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Best Local Similarity 82.6
Matches 19; Conservative
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US-418521.
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                                                                                                                     Staphylococcus aureus.
                                                                                                                                                                                                                                                                   07-JAN-1997; 100117
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09-SEP-1983; U
15-SEP-1982; U
                                                                                                                                                                                                                                         EP-786519-A2.
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                                                                                                                                                   misc_feature
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N40312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mew isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
(1aim 1, Page 593-597; 1150pp; English.
X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detection diseases related to Borrella infections in animals, and for the production of biosynthetic products such as enzymes.
Sequence 6422 BP; 1848 C; 1547 G; 1361 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1999 (first entry)
Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal;
Treponema pallidum.
Treponema pallidum.
W09859034-A2.
                                                                                                                                                        Example; Page 48; 53pp; English.

By interferon gene and method for the prodn. of interferon in yeast by use of recombinant DNA segment contg. suc 2 promoter linked to interferon gene. The interferon synthesis can be regulated over a broad range by changes in the culture medium, e.g. synthesis is repressed in glucose medium and de-repressed when glucose is depleted. Also claimed is yeast strain ATCC 20644-GG1144.

Sequence 1253 BP; and a sequence 1253 BP; seat strain ATCC 20644-GG1144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-WAR-1999 (first entry)
Enterococcus faecalis genome contig SEQ ID NO:159.
Enterococcus faecalis; contig; detection; Enterococcus infection; vaccine; attenuation; computer readable medium; ds.
Enterococus faecalis.
                                                                                                                                         Prodn. of interferon in yeast - by use of recombinant DNA segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
(COLB ) COLLABORATIVE RES INC.
Botstein D, Bowden DW, Davis RW, Fink GR, Knowlton RG,
Mao J, Taunton-Rigby A, Vovis GF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17; DB 1
Pred. No. 42;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ed. No. 53;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1198 GCGTGCTCTACCAACTGAGCTATGC 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAGCTIGITCIACCACCIGAACIAG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AAGCTTGGTCATCCATCTGAACCAG 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X13096 standard; DNA; 8160 BP. X13096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X20576 standard; DNA; 6422 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-1997; US-050667.
(HUMA-) HUMAN GENOME SCI INC.
Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                             WPI; 84-088509/14.
P-PSDB; P40741.
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useful for dia nosis and treatment of hepatic disease and
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V78290
                                                                                                                                                                                                                                                                                                                                                           RESULT 13
V79270
    F F S C C C S
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                                                                                                                                                                                                                                                                Claim 1; Page 898-902; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer based system commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus infection in an animal and monitoring modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences
                                                    14.NOY-1997; US-066009.

16.MAY-1997; US-044001.

16.MAY-1997; US-044001.

16.MAY-1997; US-044001.

16.MAY-1997; US-044001.

18.MAY-1997; US-044001.

Barash SC, Dillon PJ, Runsch CA;

WPI; 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides

used to develop products for the detection of Enterococcus and for used in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JAN-1993 (first entry)
Encodes exons XV to XVIII of human hepatocyte growth factor.
HGF: enhance growth; preparing transgenic animals; hepatic disease;
elinical diagnostic reagent; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2292 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 8160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1463 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.2%; Score 16.8; 90.0%; Pred. No. 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "exon XVIII"
7492. 7497
/*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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3764. .3937
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/note= "exon XVI"
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/*tag= a
/note= "exon XV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2731 A;
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ID 026727 standard; DNA; 7753 BP.

AC 026727;
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.879
/*tag= h
/nots
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19-NOV-11990; 314548.
19-NOV-1990; JP-314548.
(NAKA.) NAKAMURA T.
(TOYM) TOYOBO KK.
WPI; 92-265591/32.
P-PSDB; R25692.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 991.
                                       04-MAY-1998; U08985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8160 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection.
                                                                                                                                                                                                                                                     infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Table 3. Section 1. Complete in the control of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus contig SEQ ID #4959.

Computer readable medium: vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                human hepatocyte growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                          2766 T;
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                                                                                                                                                                                                                                                                                                               DB 1; Length 753;
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Pred. No. 43;
0; Mismatches 4; Indels
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07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                          1243
                                                                                                                                                                                                                                                                                                                                                                                 4;
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useful for and more transgent annual prepn.
transgent annual prepn.
Jubiclosure; Page 22; 28pp; Japanese.
This sequence contains exons XV to XVIII of factor. See also R25676-92, Q26713-27.
7753 BP; 2567 A; 1177 C;
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                                                                                                                                                                                                                                                                                                   61.5%; Score 16.6; D
82.6%; Pred. No. 84;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6273 ACCCTGTTCTACCACCTAAAATA 6251
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AGCTTGTTCTACCACCTGAACTA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 TIGCTCTACCAATIGAGCTAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V79270 standard; DNA; 59 BP.
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82.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                       Query Match 61.5
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  computer readable medium.
Sequence 59 BP; 16 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 61.5
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
EP-786519-A2.
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Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of

Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,

WPI; 97-374922/35.

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WPI: 97-374922/35.
Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
claim 1; Page 2772-2773; 3271pp; English.
This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                               /*tag= a //note= "these bases represent a line of missing text in /note= "these bases represent in the specification. They are included to maintain the nucleotide numbering given in the specificatio. for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S. aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus contig SEO ID #3947.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
Stabhylococcus aureus.
EP-786519-A2.
                              Staphylococcus aureus contig SEQ ID #3979.

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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0
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                                                                                                                                                                                                                                                                                                                                                                 05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.6; DB; Pred. No. 56; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 C;
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 TIGCTCTACCAATIGAGCTAGGC 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V78258 standard; DNA; 361 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-1997.
07-JAN-1997, 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.5%;
82.6%;
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                 .6-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.5
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                              Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                  07-JAN-1997; 100117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400 BP;
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable for the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access nemory (RAM), read-only memory (ROM) or CD-ROM. Homoloav searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are industrial importance can be obtained. Specifically, sequences which are be used in a vaccine composition against S.aureus in sample. S.aureus is a sample. S.aureus is a sample and against S.aureus in a sample. S.aureus is implicated in numerous human diseases, scholang cellulitis, eyelld infections, food poisoning, osteomyelitis, concluding cellulitis, eyelld infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used (and their fragments) are useful as primers or probos for isolating concluding cellul as primers or probos for isolating concluding contained on the concent of the solatones contained on the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.6; DE
Pred. No. 55;
0; Mismatches
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82.6%;
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Best Local Similarity 82.6
Matches 19; Conservative
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                           9; Search time 1405 Seconds
(without alignments)
37.906 Million cell updates/sec
    Compugen Ltd.
GenCore version 4.5
Copyright (c) 1993 - 1998 Comp
                                                                         2546578 seqs, 986266752 residues
                                                       1 AAGCTTGTTCTACCACCTGAACTAGGC 27
                           September 18, 1999, 06:47:49
                  - nucleic search, using sw model
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em_est11:*
em_est13:*
em_est13:*
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Perfect score:
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N88530 K3598F Huma
                                                                                                                                          H51722 yp85e07.rl<sup>-</sup>
Al045851 Homo sapi
              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                Description
                                                                                                                                                   ALIGNMENTS
                        SUMMARIES
                                   N88530
AA607268
AA331881
AA422885
AA824084
A1161663
T15736
F13213
T60600
AA004244
                                                                                                     AA307495
AA310973
AA311686
AA314612
AA316439
AI558192
C96306
C96449
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AI566060
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AA300763
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AA307033
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AI558929
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em_est26:*
                                    DB
                               Length
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Match
                                   54:
55:
57:
58:
                               Score
                                    999888999999
                                                 18.
18.
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N88530 405 bp mRNA EST 02-APR-1996 K3598F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K3598 5', mRNA sequence. 91441732 N88530.1 GI:1441732

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1. .459
/organism="Mus musculus"
                                                                                                                                                                        /strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:1005753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 432.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCTTGTTGTCCCACCTCACCTAG 264
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84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 68.9
Best Local Similarity 84.0
Matches 21; Conservative
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AA681861/c
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JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[ (bases 1 to 525)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/lab_host="Tector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
Xho!; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a Xho!-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with Xho!, for directional cloning into
predigested lambda ZAP Express."
113 9 80 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA607268 525 bp mRNA EST 30-SEP-1997 vm92h05.rl Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:1005753 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 405)
                                                                                                                                                                                                             Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Fax: 416978550
Email: liewcc@utcc.utoronto.ca
Seq primer: GAAATTAACCTCACTAAAGGG.
10.405
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="K3598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                   cDNAs from fetal heart (1996)
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GCTTGTTCTACCACCTGAACTAGGC 27
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                                            Homo sapiens
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Matches 21; Conserv
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                      human.
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JOURNAL
COMMENT
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qq δ

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/note="Organ: embryo; Vector: pSPORT; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: Sal1(dt): 5'-CGTCGACCGTCGACCGTTTTTTTTTTTTTTTT' CDNAS were cloned into the Not1/Sal1 sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 459)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MOI:569969
High quality sequence stop: 472.
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WashU +HHMI Mouse EST Project
Mashington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vr44a05.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:1123472 5', mRNA sequence.
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Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1392950.
                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib-"Knowles Solter mouse blastocyst Bl"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host-"DH10B"
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Pred. No. 55;
                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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AA422885
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DEFINITION
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AA422885
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                                                                FEATURES
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Heddlom, E., Hinkle, F. S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L. I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, W.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:1123472"
/clone="IMAGE:1123472"
/clone="IMAGE:1123472"
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/lab_brost="ballob"
/note="Organ: embryo: Vector: pBluescribe (modified);
Site_1: MluI; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 13.500 2-cell stage embryos. Primer: SalI(dI): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTT-3'.
were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA331881 224 bp mRNA EST 21-APR-1997 EST35751 Embryo, 8 week I Homo sapiens cDNA 5' end similar to similar to MER5 protein, mRNA sequence.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 224)
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Other_ESTs: THC170844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18.6; DB 37; Length 459;
Pred. No. 54;
0; Mismatches 4; Indels 0
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112 c 101 q
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AA331881.1 GI:1984123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.9%;
84.0%;
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Best Local Similarity 84.0
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bioinformatics
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AUTHORS
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MEDLINE
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1 (bases 1 to 564)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                    /organism="Homo sapiens"
/organism="ATCC (inhost):133506"
/db_xref="taxon:9606"
/clone_lib="Embryo, 8 week I"
/dev_stage="embryo, 8 wks"
/note="Organ: Embryo, 8 weeks; Vector: pBluescript SK-;
Site_l: EcoRI; Site_2: XhoI"
a 60 c 60 g 56 t 6 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA422885 564 bp mRNA EST 16-OCT-1997 vd47c06.sl Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:803722 5' similar to gb:X64550 M.musculus mRNA for hyaluronan-mediated motility (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodenija; Sciurognathi; Muridae; Murinae; Mus.
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On May 8, 1995 this sequence version replaced gi:800408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Sorest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Score 18; DB 32; Length 224; 77.8%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Knowles_Solter mouse 2 cell"
/tssue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH108"
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seg primer: M13 Reverse.
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 441.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 AAGCTCGTTCTTCCACATGCAGNAGGC 123
                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAGCITGITCIACCACCIGAACIAGGC 27
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Best Local Similarity
Matches 21; Conserv
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Query Match 66.7
Best Local Similarity 80.8
Matches 21; Conservative
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Best Local Similarity
Matches 19; Conserv
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AI161663/c
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DEFINITION
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COMMENT
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SOURCE
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Rodentia: Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 422)
Marray M. Hillier, L. Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marray M., Hillier, L., Allen, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: embryo; Vector: pBluescribe (modified);
Site_1: MluI; Site_2: SalI; Cloned unddirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI(dI): 5'-CGGTCGACGTGTTTTTTTTTTTTTT-3'. CDNAs
were cloned into the MluI/SalI sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."
mRNA prepared from 13,500 2-cell stage embryos. Primer: Sall(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTTTTT.3'. cDNAs were cloned into the Miul/Sall sites of a modified pbluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) fo: further information.
MGI:614940
                                                                                                                                                                                                                                                                                                                                                                                                                                  AA824084 422 bp mRNA EST 17-FEB-1998 vx66c03.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:1125604 5' similar to 9b:X64550 M.musculus mRNA for hyaluronan-mediated motility (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1404594.
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Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                           Length 564;
                                                                                                                                                                                                         66.7%; Score 18; DB 33; Length 56
80.8%; Pred. No. 1.1e+02;
ive 0; Mismatches 5; Indels
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/clone=lib="knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
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The WashU-HHMI Mouse EST Project
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             176 ATCTTGTTCTGGCAGCTGAACTTGGC 201
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Populus tremula x Populus tremuloides.

Populus tremula x Populus tremuloides

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Buphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.

I (bases I to 465)

Sterky,F., Regan,S., Karlsson,J., Hertzberg,M., R., ide,A., Holmberg,A., Amin,B., Bhalerao,R., Larsson,M., villarroel,R., Van Montagu,M., Sandberg,G., Olsson,O., Teerl,T.T., Boerjan,W., Gustafsson,P., Uhlen,M., Sundberg,B. and Lundeberg,J. Gene discovery in the wood-forming tissues of poplar: Analysis of 5,692 expressed sequence tags

NL Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
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/db_xref="taxon:47664"
/cloo_lib="Hybrid aspen plasmid library"
/tissue_type="Cambial region"
/dev_stage="1.5 m actively growing tree"
/lab_host="E.coli"
/note="Vector: PBluescript SK; Site_l: Sall; Site_2: NotI;
/note="Vector: pBluescript SK; Site_lisall; Site_2: NotI;
/note="Vector: pBluescript SK; Site_3: NotI;
/note="V
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A004P75U Hybrid aspen plasmid library Populus tremula x Populus
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Royal Institute of Technology (KTH)
Teknikrin en 34, S-100 44 STOCKHOLM, Sweden
Tel: +46 8 790 8287
Fax: +46 8 24 54 52
Email: fredrik@biochem.kth.se
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66.7%; Score 18; DB 39;
80.8%; Pred. No. 1e+02;
tive 0; Mismatches 5
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Seq primer: GGTTGTAAAACGACGGCAGHigh quality sequence stop: 465.
Location/Qualifiers
                                                                                                                                                                                                                                                                               182 ATCTTGTTCTGGCAGCTGAACTTGGC 207
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Washington University School of Medicine
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                                                                       T05736 337 bp mRNA EST 30-JUN-1993 EST03625 Fetal brain, Stratagene (cat#936206) Homo sapiens CDNA clone HFBDF63 similar to Retrovirus-related pol polyprotein, mRNA
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(bases 1 to 308)

(bases 1 to 308)

(bases 1 to 308)

Devignes, M. D., Duprat, S., Houlgatte, R., Jumeau, M. N., Lamy, B.,

Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Poullot, Y.,

Sebastiani Kabaktchis, C. and Tessier, A.,

IMAGE: molecular integration of the analysis of the human genome and its expression
                                                                                                                                                                                                                                          Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Ve:tebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 337)
Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.
3,400 expressed sequence tags identify diversity of transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="HFBDF63"
/clone=lib="Fetal brain, Stratagene (cat#936206)"
/clone_lib="Fetal brain, Stratagene (cat#936206)"
/note="Vector: LambdaZAP-II] 7-18 wk gestation, femalongo-dr + random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb average inser size:

a 70 c 68 g 94 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 bp mRNA EST 14-MAR-1995 normalized infant brain cDNA Homo sapiens cDNA clone
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.5e+02;
0; Mismatches 5; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                        Other_ESTs: EST03626
Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="ATCC (inhost):82427"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                       Nature Genet. 4, 256-267 (1993)
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1. .337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
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80.0%;
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T05736.1 GI:316886
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F13213.1 GI:709258
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Best Local Similarity 80.0
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                       from human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 3018699056
Fax: 3018699423
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                                                                                                                                sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 526)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chiss.e.S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hultman,M., Kucaba,T., Lacy,M., Le,M., De,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trayaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
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IMAGE:78584 5' similar to gb:K01763 HAPTGGLOBIN-1 PRECURSOR
(HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-1995
                                                    Contact: Genethon
Genexpress Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                       Tel: 33169472800
Fax: 33160778698
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human.
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                                                                                                                                                source
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ORIGIN
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                      FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                            High qality sequence stops: 283 Source: IMAGE Consortium, LLNL This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1027 Std Error: 0.00 Seq primer: M13RP1 Std Error: 0.10 High quality sequence stop: 283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_atge="149 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: liver; Vector: Peluescript SK; Site_l:
/note="Organ: liver; Vector: Peluescript SK; Site_l:
CORI; Site_2: XhOI; Cloned unidirectionally. Primer:
Oligo dT. Hepatectomy from normal male caucasian. Average sincert size: 1.1 kb. Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAGAG, 3' -3' adaptor sequence: 5'
CTCGAGITTTTTTTTTTTTTTTT. 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AANU4244 425 bp mRNA EST 07-MAY-1997 zh88d06.rl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens CDNA clone IMAGE:428363 5' similar to contains element MER22 repetitive element; mRNA sequence.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 425)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Glissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Le,N.
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Travaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.2%; Score 17.6; DB 21; Length 526; 83.3%; Pred. No. 1.6e+02; Live 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:498329"
/db_xref="taxon:9606"
/clone="IMAGE:78584"
/clone=lib="$tratagene liver (#937224)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 g
                Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1027
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20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Marra, M.
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ORIGIN
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MEDLINE
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata: Mammalia;
Eutheria: Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 480)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lecy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation and analysis of 280,000 human expressed sequence tags
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 673 Std Error: 0.00 Seq primer: mob.REGA+ET Seq primer: mob.REGA+ET High quality sequence stop: 395.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On May 9, 1995 this sequence version replaced gi:802992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.6; DB 27;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                       /db_xref="GDB:1328132"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 AAGCCICTICTACCACCIGATCAA 60
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AA004527.1 GI:1448104
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Marra, M.
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SOUTH

FEATURES

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Anote-Torgan: Kidney; Vector: p7713D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1333911, 1456007-1456775, and Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV046966 226 bp mRNA EST 18-MAY-1999
AV046966 Mus musculus adult C57BL/6J testis Mus musculus cDNA clone
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Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Ito, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H. Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Tominaga, N., Watanabe, S., Yagame, M., Tamanura, Y., Tokota, T., Yokota, T., Yokota, T., Yokota, T., Yokota, T., Yokota, T., Yokota, T., RIKEN Mouse ESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 226)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Jun 22, 1998 this sequence version replaced gi:3247120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.2%; Score 17.6; DB 48; ilarity 83.3%; Pred. No. 1.7e+02; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 t
                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                               High quality sequence stop: 459
                                                                                                                                                                                                            /clone="IMAGE:2172055"
       Seq primer: -40UP from Gibco
                                                                                  Location/Qualifiers
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Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fatima Bonaldo.
132 c 1(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV046966.2 GI:4866631
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Fax: 81-298-36-9098
                                                                                                                                                                                  /map="16"
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Matches 20; Conserv
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AV046966
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SOURCE
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                                                                                FEATURES
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                                                                                                                                                                                                                                                                                                                    John Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI566060 593 bp mRNA EST 12-MAY-1999 th 52h04.xl NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:2172055 3/similar to 9b:L1987l TRANSCRIPTION FACTOR ATF-3 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutharia: Primates: Catarrhin: Hominidae; Homo.

1 (bases 1 to 593)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 688 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 378.

Location/Qualifiers
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Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3137546.
                                                                                                                                                                                                                                                                             /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
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                                                                                                                                                                        /db_xref="GDB:1328401"
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/clone="IMAGE:428632"
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                                                                                                                                                   /organism="Homo sapiens"
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g4524512
AIS66060.1 GI:4524512
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Query Match

Matches

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BASE COUNT

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LOCUS

ACCESSION

NID VERSION

RESULT 1: AI566060

ORGANISM

KEYWORDS

SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL COMMENT

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Gaps

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Oda, H.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: Lafmid BA; Site_1: Not I; Site_2: Hind III; Size-selected cDNA from polyA+ RNA from human brain. Size-selected cDNA from polyA+ RNA from human brain. Amonth old neonate.This library is the result of an attempted normalization of library b4HB3MA."
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Columbia University
Department of Psychiatry,722 W 168th Street, Unit #41, New York,NY
10032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Construction and characterization of a normalized cDNA library Proc. Natl. Acad. Sci. U.S.A. 91, 9228-9232 (1994) 95023884
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 399)
Soares, M.B., Bonaldo, M.F., Jelenc, P., Su, L., Lawton, L and
Efstratiadis, A.
                                                       /organism="Mus musculus"
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/tissue_type="adult"
/dev_stage="testis"
/dev_stage="testis"
/dev_stage="testis"
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/clone_lib="b4HB3NA Cot8-HAP-Ft213"
/lab_host="E. coli"
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Fax: 2127813577
Email: cuc@cuccfa.ccc.columbia.edu
sense, Ampicillin
Seg primer: M13 Reverse.
Location/Qualifiers
further details.
Location/Qualifiers
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Matches 20; Conservative
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Search completed: September 18, 1999, 06:47:49 Job time: 3666 sec AC005884 Homo sapi U17165 Cricetulus

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched: Database

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AF099256 Pseudonous 267750 S.cerevisia X04246 Yeast CCC9 Z14213 S.cerevisia X68020 S.cerevisia X68020 S.cerevisia X68020 S.cerevisia AC00025 H.sapiens g AL02476 Human DNA AC00027 Human DNA AC000027 Homo sapi AC007254 Homo sapi AC007253 Arabidops AL021367 Human DNA AL021367 Human DNA AL021367 Human DNA AL021367 Human STST, M97168 Homo sapien AC005291 Human X157 M97168 Homo sapien AC005391 Homo sapien AC005031 Homo s
  X03833 Human gene
AL078622 Homo sapi
E05467 DNA sequenc
236077 S.cerevisia
M64926 Yeast urea
AL031347 Human DNA
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Y10532 S.mitis pbp
AC007140 Homo sapi
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JE 1 (Dassified.

S Kornman, K. S. and Duff, G. W.

Detecting genetic predisposition to periodontal disease

AL Patent: US 5686246-A 2 11-NOV-1997;

Location/Qualifiers

Location/Qualifiers
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HS323M22
HS3C000356
HSIGLV311
AC000027
AC003988
AC006007
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Sequence 2 from patent US 5686246.
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AC005223
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HS447D17
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HSDJ93K22
AC005302
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SCCDC9
SCYDL165W
SCSFAARP
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SCYBR208C
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HS596H12
AC005884
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       GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                    679419 seqs, 1590154680 residues
                                                  nucleic search, using sw model
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23-DEC-1997

Score

Result No.

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Direct Submission

L Submitted (11-JUN-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires:

Lumbridgeshire, CB10 1SA, UK. E-mail enquires:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

IMPORTANT: This sequence is unfinished and does not necessarily

represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished: dJ92537 Contig_ID: 01919 acc=AL078622

Length: 13921 bp Unfinished: dJ92537 Contig_ID: 02005

acc=AL078622 Length: 16691 bp Unfinished: dJ92537 Contig_ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA HTG 11-JUN-1999
22 clone DJ925J7, WORKING DRAFT SEQUENCE,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 118605)
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95.0%; Pred. No. 2.6;
tive 0; Mismatches 1;
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11863. .11970
/note="Alu repetitive sequence"
1 2489 c 2226 g 3547 t
                                                                                                                                                                                repetitive sequence"
                                                                                                                                                                                                                                                                                                                                                                                                          /note="poly(dA-dC] tract"
8912. 9137
/note="5x 46 bp repeat"
9770. 9806
/note="poly [dT-dG] tract"
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/note="poly [dA-dC] tract"
7815. .7939
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in unordered pieces.
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HTG; HTGS_PHASE1.
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/note="Alu re
6262. .6432
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4893. .517
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Best Local Similarity 95.0°
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/db_xref="GI:33786"
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DSEEEIIKPRSSPFSFLSNVKYNFMRIIKYEFILNDALNQSIIRANDQYLTAAALHNL
DEAVKFDMGAXKSSKDDAKITVILRISKTQLYVTAQDEDQPVLLKEMPEIPKTTTGSE
TRULFFWETHGTRNYFTSVAHPNLFIATKQDYWVCLAGGPPSITDFQILENQA"
/number=2
                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 11970)
Furutani,Y., Notake,M., Fukui,T., Ohue,M., Nomura,H., Yamada,M. and
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Data kindly reviewed (10-NOV-1986) by Y. Furutani.
Location/Qualifiers
1. 11970
                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete nucleotide sequence of the gene for human interleukin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254. 393
/note="Alu repetitive sequence"
1375. 1382
/note="direct repeat 1"
1375. 1390
/note="pot. transcription activator (seq. homolog. to adenovirus 2 major late promoter transcription factor
                                                                                                                                                                                                                                           7303833.1 GI:33785
Alu repetitive sequence; interleukin 1 alpha; inverted repeat;
repetitive sequence.
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6262. .6432,7815. .7939,10290. .11643)
1489. .2152
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/codon_start=1
   Gaps
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X03833
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/note="inverted repeat A'"
1383. 1390
/note="direct repeat 1"
 Mismatches
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1375. 1382
/note="inverted repeat A"
1383. 1390
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/number=2
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24-SEP-1993;
24-SEP-1993;
PF 05-MAR-1920 44531
PF 05-MAR-1920 44531
PI NISHTA YOSHBAKI, SOGABE YUKIHIRO, AISUI SHIGENORI PC C12N15/60,C12N1/19, PC C12N15/60,C12R1:865), (C12N1/19, PC C12N1865);
CC Strandedness: Double;
CC Strandedness: Double;
CC Actionly Linear;
CC Hypothetical: No;
CC Anti-sense: No;
CC **Source: strain-ATCC44769;
FH Key Location **
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00363 acc-AL078622 Length: 27242 bp Unfinished: dJ925J7 Contig_LD: 001058 acc-AL078622 Length: 56385 bp Unfinished: dJ925J7 Contig_LD: 00726 acc-AL078622 Length: 1166 bp. * NOTE: This is a 'working draft' sequence. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                              Length 118605;
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27752 c 27696 g 30563 t
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Best Local Similarity 94.4%; Pred. No. 36;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                              84.0%; Score 16.8; Dilarity 90.0%; Pred. No. 24; Conservative 0; Mismatches
                                                                                                Location/Qualifiers
1. 118605
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/chromosome="22"
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Saccharomyces cerevisiae.
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OVABLEDPTVISILEGAKKY SAVOCFSFEYKROGILOKVRRILESSVOALOSFLDSKPP
KESLDPTVISILEGAKKY SAVOCFSFEYKROGILOKVRRILESSVOALOSFLDSKPP
QOVABLEPLVLNNSROGTWINRYNLADLAALAAPAGFRDDGEDMGITLIGKKFTDYALLE
LANNYFONIFPNGSRTYGTETSSSYKRANDOLVGPDYDSTSIKLAVVGAHLKGLPLE
LANNYFONIFPNGSRTYGTETSSSYKRANDOLVGPDYDSTSIKLAVVGAHLKGLPLE
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KESOKKKLEDTVLIANRGEIAVRIIKTIKKGIRSVAVYSDPDKYSQHVTDADVSVPL
IRGIGLKHSAROJAGKAGVPLYPGSLLITSYEEAKKVAAELEYPWWYSTAGGGIGL
OKUDSEEDIEHIFETVKHOGET FFCDAGVELER IERNARHVEVQLMGOGFRAILHGE
ROCSLOKRNOKVIEETPARHOFFFTEDAGVELER IERNARHVEVQLMGOGFRAALAGE
FYLEEVNTRLOVBETTAANNYGLDLVEWMIRIAANAPDFDSTKVEVNGVSMEARLY
ENPLINTELOVBETTAANTGLDLVEWMIRIAANAPDFDSTKVEVNGVSMEARLY
ENPLINTERSPEGLLVDVKFDDAANAVOTWKKGTNISPSTYDPTLATTLYDGAH
TSIQDYGGRYGCTITNDYKESTITSDFFRKANSTSTNILMSSYQYEPTAIETTLPGAH
TSIQDYGGRYGVENTLGOPPSSTLITSDFFRKANSTSTNILMSSYQYEPTAIETTLPGAH
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TSIGTALCTLDGQEIPQHYKYDVENTSSTLISGFRANSTNIGGEGGHH
FSITTGGTALCTLDGQEIPQHYKYDVENTSSTLISGFRANSTNIGGEGGHH
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PSINTHUSYYSLGGANNATGENSTLICTGGSSTLISGFVCOAVUPDERLENTGENSTRICTGGSTUP
                                                                              VAPVDNAMICLISKENLLHOFQILKSRENKETLPLYCOPIAVKDNIDVRGLPTTAACP
SFAYEPSKDSKVVELLRNAGAIIVGKTNLDQFATGLVGTRSPYGKTPCAFSKEHYSGG
SSAGSASVVARGIVPIALGTDTAGSGRVPAALNNLIGLKPTKGVFSCOGVVPACKSLD
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YRQAGDKYVLVLEXGONELTENBISYERELLISLYKKKRTGTTGYVENGGOVRSVLIEFDG
YKYTQKELLKVLVAFTEIGPEGFRITSNII RLPMAFEDSKTLACVQRYQETIRSSA
PWLENNVDEIANVNGIERNEVY JALYSARFMYLGLGDVFLGSPCAVPLDPRHFRLGSK
                                                                                                                                                                                                                                                 CVSIFALNLSDAERCFRIMCOPDPDNDEYSRPYVSNPLKKFSSNVTIAIPKNIPWYGE
                                               /translation="MTVSSDTTAEISLGWSIQDWIDFHKSSSSQASLRLLESLLDSQN
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[ Chases I to 6141)

[ Chases I to
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1313 c 1099 q 1810 t
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Yeast urea amidolyase (DUR1.2) gene, complete cds.
M64926
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    .6141
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/db_xref="taxon:4932"

db_xref="SWISS-PROT:P32528"
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241. .5748
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KESLDPTVISTIEGARKY SANDCFSFER KROGILOKVRRLLESVOULCVPTCPLIDARP
KESLDPTVISTIEGARKY SANDCFSFER KROGILOKVRRLLESVOULCVPTCPLINFT
QOVADEPVLVINSROGTWITNFVNLADLAALAVPAGFRODGLPWGILLTGKKFTDYALLE
LANRYFONMFPNGSRTYGTFTSSYKRANDOLVGPDYDPSTSIKLAVVGAHLKGLPLH
WOLEKVNATYLCTTKTSKAYOLFALPKNGPVLKPGIRRYODSNGSOIELEVYSYPKEL
FGAFISMVPEPLGIGSVELESGEWIKSFICEESGYRAKGTVDITKYGGFRAYFEMLKK
KESOKKKLEDTVLIANRGETAVRIIKTLKKLGIRSVAVYSDPDKYSOHVTDADVSVPL
HGTTAAOTYLDMNK ILDAAKOTNAOAIIPGYGYGELSRAMSTSAOITFYGRSGDI
IRGLGIKHSARQIAOKAGVELVPGSLLITSVERAKVAAELEYPVWYKSTAGGGGIGL
OKVDSEEDIEHIFETVKHQGFFFGDAGVFLKRFIENARHVEYQLMGDGFGRAIALGE
RDCSLOKRNOKYVIETPPAMLPEKTRLLRKAAESLGSLLNYKCAGTVFFTYDEKKDE
FYELEVNTRLOVEHPITEMYTGLDLVEWMITIAANDAPPDEDSTYVOLNGOGFGRAIS
KLNOALEETKYYGCITNIDYLKSIITSDFFAKRVSTNILNSYQYEPTAIEITLPGAH
TSIODYPGRVQTWRICVPPSOMDAYSFRLALRKAVSTNILNSYQYEPTAIEITLPGAH
TSIODYPGRVQTWRICVPPSOMDAYSFRLALRKAVSTNILNSYQYEPTAIEITLPGAH
TSIODYPGRVQTWRICVPPSOEDMAYSFRLALRKAVSTNILNSYQYEPTAIEITLPGAH
TSIODYPGRVQTWRICVPPSOEDMAYSFRLANRIVGONDYRPRAPAISGIRGIDVPKYL
GSYSTFLIGNVGGYNGRVLKLDSVERSTLSIKKHYNSNRFGVRIGTREWR
IGVTCGPRGSPFFRRESIEEFFRESERWKWHYNSNRFGVRIGTREWR
                                                                                                                                                                                                /translation="MTVSSDTTAEISLGWSIODWIDFHKSSSSQASLRLLESLLDSQN
VAPVDNAWISLISKENLLHQFOILKSRENKETLPLYGVPIAVKDNIDVRGLRTTAACP
SFAYEPSKDSKVVELLRNAGAIIVGKTNLDQFATGLVGTRSPYGKTPCAFSKEHVSGG
SSAGGASVVARGIVPIALGTDTAGSGRVPAALNNLIGLKPTKGVFSCQGVVPACKSLD
                                                                                                                                                                                                                                                                                                                                       CVSIFALNLSDAERCFRIMCQPDPDNDEYSRPYVSNPKKNFSSNVTIÄ PKNIPWYGE
TKNPVLFSNAVENLSRTGANVIEIDFEPLLELARCLYEGTWVAERYQAIQSFLDSKPP
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VYRQAGDRYVLVEYGDNEMNFNISYRIECLISLVKKNKTIGIVEMSQGVRSVLIEFDG
YKVTQKELLKVLVAYETEIQFDENWKITSNIIRLPMAFEDSKTLACVQRYQETIRSSA
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LGERAEEFAKLIQNANSELKESVIVKPDEEEDFPEGAEIVYSEYSGRFWKSIASVGDV
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Human DNA sequence from clone 596H12 on chromosome 6p22.2-22.3.
Contains ESTs, STSs and GSSs, genomic marker D6S461 and TC, CA and
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Submitted (23-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175555)
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82.0%; Score 16.4; DB 8; Length 6141;
Best Local Similarity 94.4%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 1; Indels 0;
                            /evidence-experimental
/product-"urea amidolyase"
/protein_id="And1643.1"
/db_xref="PID;9173122"
/db_xref="G1:173122"
/function-"hydrolysis
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requests: clonerequest@sanger.ac.uk
on Jan 16, 1999 this sequence version replaced gi:3927943.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence is the entire insert of clone 596H12. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          igger3(Golem) repeat: matches 2. .142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                         This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 human chromosome 6, constructed by the Sanger Centre Chromosome 6 http://www.sanger.ac.uk/HGP/Chr6 596H12 is from the library RPC14 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167. 4545
note="HERV16 repeat: matches 1571. .1944 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7293. .6503 --reconstruction 10/1. .1944 of consensus' note-"HERVL repeat: matches 4443. .4661 of consensus" 1087. .7374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9910. .3374

Mote-#LDPA2 repeat: matches 5669. .6146 of consensus"

1787. .4161

Mote-#LIPA7 repeat: matches 5771. .6142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .940 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2780. .13027]
fnote="LIME repeat: matches 5533. .5788 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1540. 1928

Anote-"LTR16A repeat: matches 18. .440 of consensus"

1230. .2825

Anote-"HER16 repeat: matches 328. .940 of consensus'

1910. .3374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Alujb repeat: matches 1. .289 of consensus" 492. .7746
note="LIR16A repeat: matches 25. .291 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="Tigger3(Golem) repeat: matches 2781. .3038 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8762. 8831
Moote-"MSTA repeat: matches 361. .426 of consensus"
8832. .9142
Moote-"Alusg repeat: matches 1. .313 of consensus"
9143. .9475
Moote-"MSTA repeat: matches 1. .361 of consensus"
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/note="match: GSS AQ219540"

9884. .10190

/note="AluSg repeat: matches 1. .308 of consensus"

complement(11134. .11527)

/note="match: GSS AQ086021"

complement(11525. .11848)
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/note="L2 repeat: matches 972 .1381 of consensus"
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Mote="MIR_repeat: matches 8. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    913. .8039
.note-"LTR16A repeat: matches 317. .442 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note-"match: GSS A0062320"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="p22.2-22.3"
/clone_lib="RPCI4"
710. .840
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                                                                                                                                                                                                                                                                                                                                                            feature key
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repeat\_region /note="12" repeat: matches 2041. 2745 of consensus" repeat\_region /note="15" repeat matches 2041. 475 of consensus" repeat\_region | 15502. 15012 repeat\_region | 15502. 15012 repeat\_region | 1502. 1502. 1502 repeat\_region | 1502. 1502 repeat

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Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichvolsky, N., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J. and Zody, M.

Library, J. Choller, Manner, C., Lander, E., Allen, N., Anderson, M., Brearch, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 120 Charles Street, Cambridge, MA 02141, USA

Bliren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Cardia, S., Gardjary, K., Granf, G., Jacopins, C., Kann, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., McGurk, A., McKernan, K., Madchand, J.C., Jacotot, L., Jones, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Norris, W., Morrow, J., Wyssiller, H., Vo, A., Wagner, A., Wheeler, J., Wuy, Y., Wyman, D., K., Wagner, J., Lobotot, J., Wolla, M., Vo, M., Wagner, A., Waynan, D., K., Wagner, A., Waynan, J., Way, J., Waynan, J., Wayn, J., Labot, J., and Zody, M., Ve, W., Y., Wyman, D., Weller, J., Labot, J., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Only the last 120187 base pairs of this clone are being submitted. The remainder overlaps with accession number AC005856(WIGGR project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-NOV-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON NOV 10, 1998 this sequence version replaced gi:3850604. All repeats were identified using RepeatMasker: Smit, A.F.A. 6 Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone=" hRPK.264_B_14"
/clone_lib="RPCI-11 human BAC library"
/map="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136. .253
/rpt_family="MIR"
1699. .1783
/rpt_family="MIR"
complement(1997. .2070)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(6792. .6820)
/rpt_family="(CA)n"
complement(6888. .6898)
/rpt_family="Charliel"
6899. .7192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Homo sapiens"
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312. .6407
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/rpt_family="L1M4c"
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/rpt_family="AluSg/x"
6671. .6776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606
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1. .120187
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complement(6097. .6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'rpt_family="Aluy"
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197. .5497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'chromosome="17"
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JOURNAL
                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                          REFERENCE
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46198. .47354
/note="THEIC-internal repeat: matches 427. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished

2 (bases 1 to 120187)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C.,

Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K.,

Donelan, L., Ferreira, P., Fitzlugh, W., Forrest, C., Funke, R.,

Gage, D., Gardyna, S., Geraigery, K., Grant, G., Hagos, B., Heaford, A.,

Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L.,

Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P.,

McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J.,
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                            Jabels. 1288/8.

Jabels. 1288/8.

Jobels. MERSB repeat: matches 62. 120 of consensus.

Jobels. MERSB repeat: matches 9. 554 of consensus.

Jobels. MERSB repeat: matches 137. 304 of consensus.

Jobels. MERSB repeat: matches 137. 304 of consensus.

Jobels. MERSB repeat: matches 1. 722 of consensus.

Jobels. MERSB repeat: matches 69. 178 of consensus.

Jobels. MERSB repeat: matches 5555. 6325 of consensus.

Jobels. MIR repeat: matches 28. 262 of consensus.

Jobels. MIR repeat: matches 1. 167 of consensus.

Jobels. MIR repeat: matches 1. 167 of consensus.

Jobels. MERSB repeat: matches 1. 371 of consensus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17355. .47733

//otce="THEIC repeat: matches 1. .371 of consensus"

77817. .48057

//note="LIMD3 repeat: matches 7484. .7739 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Limec repeat: matches 1593. .1674 of consensus" 52472. .52566
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 120187)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone hRPR.264_B_14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51669, .51763
/note="L2 repeat: matches 2628. .2708 of consensus"
52271. .52350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA PRI 10-NOV-19
17, clone hRPK.264_B_14, complete
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/note="22 copies 2 mer gt 93% conserved"
51669. .51763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;;
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AC005884
93858902
AC005884.1 GI:3858902
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Best Local Similarity 94.4'
Matches 17; Conservative
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AC005884/c
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~v314. .20446
/rpt_family="LIMB6"
complement(21891. .22202)
/rpt_family="AluJb"
complement(2235. .22460)
/rpt_family="L2"
22461. .2276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24876. ...24901
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complement(25113. .25147)
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complement(25148. .25429)
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18854. .19070
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23054. .23085
/rpt_family="(TAAAA)n"
complement(23086. .23144)
/rpt_family="L2"
24563. .24608
/rpt_family="(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(28533. .28837)
/rpt_family="AluJo"
complement(29747. .29960)
/rpt_family="L2"
/rpt_family="L2"
/rpt_family="L2"
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/rpt_family="(CAAAA)n"
complement(14481..14764)
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/rpt_family="Charliel"
8762. .9063
/rpt_family="LIME3"
complement(9064. .9357)
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complement(28432. .28519)
/rpt_family="LiMC1"
              complement(7193. .7810)
/rpt_family="Charliel"
complement(7811. .8099)
/rpt_family="AluSp"
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26609. .26787
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27051. .27337
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                                                                                                                                                                                /rpt_family="LlME3"
9458. 9765
/rpt_family="AluSx"
9766. 10787
/rpt_family="LlME3"
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1991. .12016
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2785. 220c.
/rpt_family="AluSx"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
1 (bases 1 to 766)
Whitters,M.J. and Collins,M.
Hamster CDNA homologs to the mouse immunoglobulin kappa constant and 1gk-V 45.1 genes
Immunogenetics 42 (3), 227-228 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CMU17165 973 bp mRNA ROD 04-DEC-1995
Cricetulus migratorius Ig kappa light chain mRNA, complete cds.
U17165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (15-NOV-1994) Mary Collins, Genetics Institute, 87
Cambridge Park Dr., Cambridge, MA 02140, USA
Location/Qualifiers
1. 973
/organism="Cricetulus migratorius"
/db.xref="taxon:10032"
/dev_stage="rearranged"
50. 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 120187;
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/product='immunoglobulin kappa light chain"
/product='AAA82732.1"
/protein_id='AAA82732.1"
/db_xref="PID:g841148"
/db_xref="GI:841148"
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82.0%; Score 16.4; DB 11;
Best Local Similarity 94.4%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                 complement(34924...35228)
/rpt_family="Alusc"
3rpy_35260
/rpt_family="(TA)n"
35344...35409
/rpt_family="(TA)n"
/rpt_family="(TA)n"
/rpt_family="(TA)n"
38608...38515)
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13695. .33716
                                                              complement(31697. .31726)
/rpt_family="(CAA)n"
32265. .32298
                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="HSMAR2"
38632. 39098
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39099. 39409
/rpt_family="Aluy"
39410. 40054
                                                                                                                                                                               /rpt_family="AT_rich"
34886. 34928
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            /rpt_family="L1MC5"
31072. .31236
/rpt_family="MER5A"
                                                                                                                  'rpt_family="(TA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 973)
Collins,M.
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U17165.1 GI:841147
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baker's yeast
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/translation="MKLPVLLLALLFMIPDSRGDVVMTQSPNVLSVSLGEQVSISCR
SQSLVQSMONTYVNMFLQPRGQSPRRIJKYFRNSGVPDFEGSGSDKDFTLKISR
METBDFGGYYCMOGSVYVPMFFGPGTKLEIKRADAKPPVSIFPPSSEQLGTGSATLVCF
VNNFYPKDINVKWKVDGSEKRDGVLQSVTDQDSKDSTYSLSSTLSLTKADYERNHLYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases I to 450)
Koike, S.T., Barak, J.D., Henderson, D.M. and Gilbertson, R.L.
Bacterial blight of leek: A new disease in California caused by Pseudomonas syringae
Plant Dis. (1998) In press
2 (bases I to 450)
Barak, J.D., Gilbertson, R.L. and Koike, S.T.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group,
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SC41KCIV 41175 bp DNA PLN 10-NOV-1995
S.cerevisiae DNA (cosmid 31A2; chromosome IV; 41 kb).
267750
                                                                                                                                                                                                                                                                                                                                                              Pseudomonas syringae pv. pisi strain 539 internal transcribed
spacer 1, complete sequence.
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Davis, One Shields Blvd., Davis, CA 95616, USA
Location/Qualifiers
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89.5%; Pred. No. 69;
tive 0; Mismatches 2;
                                                                                                                                                                                 Score 16.4; DB
Pred. No. 32;
                                                                                                                                                                                                              0; Mismatches
                                                         CEVTHKTSTAAIVKTLNRNEC"
50. .391
392. .448
449. .766
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94.4%;
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1939. .3582
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                                                                                                                                           Saccharomyces cerevisiae
Sukaryota; Fungli. Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 41175)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATC GmbH,
                                                                                                                                                                                                                                                                                                                                                                                                            PODITION.

Direct Submission
Submitted (09-NOV-1995) Thomas M. Pohl, GATC Gm
Submitted (09-NOV-1995) Thomas M. Pohl, GATC Gm
Eritz-Arnold-Str. 23, Konstanz, 78467, Germany
Location/Qualifiers
1. .41175
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                                                                                                                                                                                                                                                                                                                       Unpublished 2 (bases 1 to 41175) Pohl, T.M.
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us-09-037-472-8.rge

CDS

CDS

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KKPKNKLKGKSAPPERAIGRGAGNIISPKSSRNTINHNLNDDDEDKFNLKDDNGKEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGEYHFRDGGYKHVNEPTAIASLQDTVRNKNDDSWQLYVKKEMEAIRÖCTLRGLLELD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Ferguson, J., Ho, J.Y., Peterson, T.A. and Reed, S.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLN
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Yeast cell division control gene CDC36.
X04287
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0; Mismatches
                                                                                                                                                                                      /db_xref="SPTREMBL:Q12515"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.0%; Score 15.8;
89.5%; Pred. No. 87
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CDC36 gene; cell division control.
baker's yeast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(14650. .15129)
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7; Criservative
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ACCESSION
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Matches
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KEYWORDS
SOURCE
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LNAQKRRLDYDEXDLTFIYKKVKRD*
COMPLEMENT(10527. .11561)
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SHRNGNDGVNEDDNTTDESDETWTSFLIDDYKKMDIVCIDHFVILSAFRPRYYDEPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIYCYNCGGKGHFGDDCKEKRSSRVPNEDGSAFTGSNLSVELKQEYYRHMNRNSDENE
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KLVLRPKSVEKVSLILNYCNDEKIAVVPQGGNTGLVGGSVPIFDELILSLANLNKIRD
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EEVSKILKICHDNNMPVVPFSGGTSLEGHFLPTRIGDTITVDLSKFMNVVKFDKLDL
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14234. .15121
                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative
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Mortisco more more than the cell may be implicated in the cell direct repeat elements (1) may be implicated in the cell direct repeat elements (1) may be implicated in the cell director vocal manner and a constant states (1) and more of constant states (1) and included the putative ATP binding site. Choose included within the category of so-called 'start genes', encoding proteins which are required in early G1, when the cell is faced with the option of initiating a further cell cycle.
                                                                                                                                                                                                                                                                                                            1 (bases 1 to 3849)
Barker, D. G., White, J. H. and Johnston, L. H.
The nucleoride sequence of the DNA ligase gene (CDC9) from
Saccharomyces cerevisiae: a gene which is cell-cycle regulated and
induced in response to DNA damage
Nucleic Acids Res. 13 (23), 8323-8337 (1985)
                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                          inverted repeat; unidentified reading frame.
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'note="direct repeat 1"
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/note="direct repeat 1"
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/note="direct repeat 1"
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                                                                                                                                    SCCDC9 3849 bp DNA Yeast CDC9 gene for DNA ligase.
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/db_xref="SGD:S0002324'
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/gene="CDC36"
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/gene="CDC36"
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/gene="CDC36"
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                               272 TACATATGACCATTCCATG 290
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/gene="CDC9"
         2 TACATATGAGCCTTCCATG 20
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/db_xref="FD:3491"
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/db_xref="SWISS-PROT:P06100"
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RVALEQDETLFFLFYKHPGTV1QELTYLELRKRNWRYHKTLKAWLTKDPMMEPIVSAD
RSERGSYVFFDPQRWEKCQRDFLLFYNAIM*
806. 814
/gene="CDC36"
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Nucleotide sequence of the yeast cell division cycle start genes CDC28, CDC36, CDC37, and CDC39, and a structural analysis of the predicted products
Nucleic Acids Res. 14 (16), 6681-6697 (1986)
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/codon_start=1
                                                                                                                           /organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
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893. .896
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226 c 240 g 352 t
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0; Mismatches 2;
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/db_xref="SGD:S0002324"
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/note="TATA-like sequence"
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//db_xref="SGD:S0002324"
207. 782
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/note="CAAT-like sequence"
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157. 160
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189. .192
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                                                                                           Location/Qualifiers
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/gene="CDC36"

    .1208
    /gene="CDC36"

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/gene="CDC36"
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/gene="CDC36"
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/gene="CDC36"
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/gene="CDC36"
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SESTCKEKANGOLIKUKYKUIGDIGEIAAGARNVOPTHYRENPEITVOEVENLAAIAKTI
KDSTCKKKMOLIKUKYKUIGDIGEIAAGARNVOPTHYRENPEITVOEVENLAAIAKTOG
KDSOLKKHKLIKRMITACKGIEKFLIRSLESKLRIGIAEKTVIISLEBGIALLHDENR
EDSPDKOVPHOVLESAQOKIRDAFCOVPNYEIVINSCLEHGIMNLOKYCILKREGIFIK
EINITOPIGDUTTKNILLIDCEAVAMNEDOGALILPPOVUSTRRKROVENHTERYP
EINITOPIGDUTTKNILLIDCEAVAMNEDGGKETPEPOVUSTRRKROVELINDVKWVCL
FAFDILCYNDERLINKSLKERREYLTKVTKVVPGEROYATOTTTNHUDELOKFLDESY
NHSCEGLMYKMLEGPESHYEPSKRSRNMIKKKNDYLEGVGBSLDCVLGAYYGRGKRT
GTYGGELLGCXNQDTGEFETCCKIGTGFSDEMJOLLHORLYVPT
EPDVWFEPTTLEFVLIADISLSPIYRAGSAFFDKGVSLAPFRINGSBATSSA
DOIVELYENQSHMQN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation=WERFGLKEDKELSSTYDHSWTLGADLSSWLYSLGIP
RDSQDHRVLDTFQSPWAETSRSEVEPRFFTPESFTNIPGVLQSTYTPPCFNSIQNDQO
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FTSMKNKPTEGTPSPKKSSKHMLEERMDNVSGEEEYATKKLKQTAVTHTVAAPSSMGS
NFSSIPSSAPSSGVADSPQQSQRLVGEVEDALSSNNNDHYSSNIPYSEVCEVFNKIEA
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Saccharomycetaceae; Saccharomyces.
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Submitted (09-JUL-1996) Data collected by MIPS on behalf of the
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                                                                                                                                                                                                                                                                                                                                                                             /gene="CDC36"
/note="open reading frame (CDC36) (aa 1-191)"
/codon_start="
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/protein_id="CAA27006.1"
/db_xref="pupple"
/db_xref="Tol3516"
/db_xref="SWISS-PROT:P06100"
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/db_xref="SGD:S0002324"
3142. .3144
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/db_xref="SGD:S0002324"
755 c 771 g 1158 t
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274213 Z71256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TACATATGAGCCTTCCATG 20
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2 (bases 1 to 944)
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Pohl, T.M.
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Saccharomycetaceae; Saccharomyces.
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arp gene; beta-D-galactosidase; CDC36 gene; CDC9 gene; sfa gene.
baker's yeast.
European yeast chromosome IV sequencing project. MIPS at the Max Planck Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG: E-mail: Mewes@mips.embnet.org
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Submitted (05-AUG-1992) E. Wehner, Institut f Mikrobiologie,
Theodor Steinkai 7, Haus 75, 6000 Frankfurt/Main, FRG
3 (bases 1 to 7008)
Wehner, E.
Direct Submission
Submitted (22-NoV-1994) E. Wehner, Institut f Mikrobiologie,
Theodor Steinkai 7, Haus 75, 6000 Frankfurt/Main, FRG
On Nov 28, 1994 this sequence version replaced gi:288588.
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S.cerevisiae SFA and ARP genes.
X68020 S59849
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Wehner, E.
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Best Local Similarity 89.5
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1305 c 1367 g 2070 t
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complement(565. .1140)
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2277. .4436
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BASE COUNT ORIGIN

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89.5%; Pred. No. 79;
tive 0; Mismatches
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Query Match 79.0
Best Local Similarity 89.5
Matches 17; Conservative
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Job time:
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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- nucleic search, using sw model OM nucleic September 18, 1999, 05:27:24; Search time 213.04 Seconds (without alignments) 23.488 Million cell updates/sec Run on:

US-09-037-472-8 20 1 TTACATATGAGCCTTCCATG 20 Title: Perfect score: Sequence:

IDENTITY\_NUC Scoring table:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. N\_Geneseq\_36:\* Database :

SUMMARIES

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Tija84;

Tija84;

Tija84;

Tija84;

Erimer for detecting genetic predisposition to periodontal disease.

Erimer for detecting genetic predisposition to periodontal disease.

Erimer for detecting genetic predisposition to periodontal disease.

Winterleukin-1 alpha; IL-1A; interleukin-1 beta; IL-1B; primer; PCR;

Winterleukin-1 alpha; IL-1A; interleukin-1 beta; IL-1B; primer; PCR;

Syntheric.

WO9706180-A1.

20-FEB-1995; US-510696.

REDI-1995; US-510696.

REDI-1996; US-510696.

REDI-1996; US-510696.

REDI-1997; US-510696.

REDI-1996; US-510696.

REDI-1996; US-510696.

REDI-1997; US-510696.

REDI-1997; US-510696.

REDI-1996; US-510696.

REDI-1997; US-510696.

REDI-1996; US-510696.

REDI-1997; US-510696.

REDI-1996; US-5
   Mouse semaphorin 3
DNA encoding P30a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Interleukin-1-alpha primer 4 (-888/-869).
IL-1-alpha; genetic polymorphism; PCR; primer; amplification; sight threatening diabetic retinopathy; interleukin-1-alpha; interleukin-1-beta; interleukin-18N; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 G;
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09-OCT-1997; G02790.

10-OCT-1996; GB-021129.

(DUFF.) DUFF G.

(RENN/) RENNIE I.

(RICH/) RICHARDSON R.

(ARCH/) RICHARDSON R.

WPI; 98-240835/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               п п
                                                                                                                                                                                                                                                                                                                                            T13884 standard; DNA; 20 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V32396 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 BP;
71.0
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WO9815653-A1.
14.2
14.2
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                                                                                                                                                                                                                                                                  RESULT
T13884
       44
45
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Claim 2: Page 31: 41pp; English.

Interleukin-1-alpha (IL-1-alpha) primers 4 and 3 (v32395) were used to amplify the IL-1alpha gene region to identify single base variation amplify the IL-1alpha gene region to identify single base variation of polymorphism of c/T at base 889. The invention claims to provide a method for predicting the risk of sight threatening diabetic retinopaty. The method involves isolating DNA from a patient and determining the DNA polymorphism pattern of the genes that code for interleukin-1-alpha, interleukin-1-beta and interleukin-1RN. The polymorphic pattern is thereby identifying patients carrying a genetic polymorphism patterns thereby identifying patients carrying a genetic polymorphism cascociated with increased risk of sight threatening diabetic retinopathy. The method may be able to identify diabetic patients at risk before the clinically detectable disorders occur. Polymorphism pattern cattern and in genes involved PCR reactions using primers v32389-v32389. The method is also claimed to be useful in conjunction with catering in genes involved effects. In identifying diabetic retinopathy in genomic DNA and therefore, in identifying diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New method of determining a patient's susceptibility to inflammatory disorders - by detecting the presence of an IL-1 (44112332)

Thaplotype, useful in designing treatment strategies that modulate the activity of proteins produced by the IL-1 gene cluster

Claim 3: Page 33: 49pp; English.

Claim 4: Page 4: Page
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Interleukin 1 (44112332) haplotype PCR primer #6.
Interleukin 1: IL-1; haplotype; inflammatory disorder; alopecia areata; coronary artery disease; osteoporosis; nephropathy; diabetes mellitus; Graves disease; systemic lupus erythamatosus; lichen sclerosis; ulcerative colitis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Predicting increased risk of sight-threatening diabetic retinopathy

    comprises identifying genetic polymorphism pattern for genes
    IL-1A, IL-1B and IL-1RN, useful to allow treatment before clinical

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB 1; Length 20;
Pred. No. 0.062;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patients expressing multiple risk patterns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1998.
21-MAY-1998; G01481.
29-MAY-1997; GB-011040.
(CAMP.) CAMP N J.
(COXA.) COX A.
(DGTO/) DE GIOVINE F S.
(DUFF/) DUFF G.
CAMP NJ. COX A, DE GIOVINE FS, DUFF G.
WPI: 99-080814/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Sc
100.0%; Pr
tive 0;
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X16612;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TTACATATGAGCCTTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 20, Conservative
                                                                                              symptoms occur
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Homo sapiens.
WO9854359-A1.
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         disease associated haplotype enables determination of which alleles are causative, and this information is useful in designing treatment strategies, including gene therapy and treatment using various agents that modulate the activity of proteins produced by the IL-1 gene cluster. Some alleles from the IL-1 gene cluster are associated with particular inflammatory diseases, and insufficient IL-1 production appears to act centrally in the pathology of these diseases. Therefore, the use of IL-1 gene clusters is useful in determining genetic susceptibility to liftlammatory diseases, including those with a multifactorial etiology with a multifactorial etiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                 Tango-77; human; IL-Ira; cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
 psoriasis, and insulin dependent diabetes. The identification of
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                                                                                                                                                                                        Length 20;
                                                                                                                                                                100.0%; Score 20; DB 1; Length zv.
100 0%; Pred. No. 0.062; Indels
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                                                                                                                                               7 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
H
                                                                                                                                                                                                                                                                                                                                                                      Human IL-1ra BAC contiguous DNA sequence 33.
                                                                                                                                                 3 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1238 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1998; U16102.
02-JUL-1998; US-091650.
04-AUG-1997; US-054646.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
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C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           its receptor complex.
5701 BP; 1729 A;
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0
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                                                                                                                                                                                                                                                     1 TIACATATGAGCCTTCCATG 20
                                                                                                                                                                                                                                       1 TTACATATGAGCCTTCCATG 20
                                                                                                                                with a polygenic component.
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                                                                                                                                                                                                                                                                                                                                            X02988;
22-JUN-1999 (first entry)
                                                                                                                                                 5 A;
                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 20; Conserv
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es 19; Conserv
                                                                                                                                               20 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 99-153692/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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ID Q4
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W09406913-A.

10 31-MAR-1994.

10 1-MAR-1995.

11 - SEP-1992: US-947263.

11 - SEP-1992: US-947263.

12 - SEP-1992: US-947263.

13 - SEC DEPT HEALTH.

14 - USSH ) US SEC DEPT HEALTH.

15 - WPI: 94-118462/14.

16 - WPI: 94-118462/14.

17 - Purified hepatitis E strain SAR-55 virus - used to develop prods.

17 - Tor use in detection, diagnosis, vaccines and therapy of hepatitis E virus infection

18 - SEP-1992: USB - SEP-1992: US
                                                                                                                                                                                                                                                                                                                        Gaps
                                                P-PSDB; P50361.

New peptide(s) useful in treatment of myasthenia gravis - also in diagnosis, having acetyl:choline receptor-alpha like activities. Disclosure: Fig 1: 13pp; Japanese.

Peptides derived from the hACR-alpha gene product have similar immunogenicity to the gene product, and may be useful in the treatment and diagnosis of myasthenia gravis caused by neuropathy in
                                                                                                                                                                         autoimmune reaction to ACR.
The sequence given contains breaks in some of the introns, at these locations 60 N residues have been inserted to preserve integrity. Sequence 4708 BP; 1124 A; 1059 C; 965 G; 1200 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          045197;
21-OCT-1994 (first entry)
21-OCT-1994 (first entry)
HEV strain SAR-55 cDNA sequence.
Hepatitis E virus; HEV; strain SAR-55; open reading frame; ORF;
antibody; detection, diagnosis; primates; stool suspension; ss.
Hepatitis E virus strain SAR-55.
Key Location/Qualifiers
28. 5109
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0
                                                                                                                                                                                                                                                                                     DB 1; Length 4708;
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                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                     79.0%; Score 15.8; 89.5%; Pred. No. 19;
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n= seq:tgg, aa:Tyr
.5457
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/codon=_seq:cag,
misc_difference 4081. .4083
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5011. .5013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon= seq:ggc,
5147. .7129
05-OCT-1983; JP-186402.
(MITU ) MITSUBISHI CHEM IND KK.
WPI; 85-144120/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q45197 standard; cDNA; 7168 BP
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//abel= ORF-2
misc_difference 5780. .5782
/*tag= 9
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/label= ORF-3
                                                                                                                                                                                                                                                                                                                                                                              1164 TGACAGATGAGCCTTCCAT 1146
                                                                                                                                                                                                                                                                                                                                                           1 TIACATATGAGCCTTCCAT 19
                                                                                                                                                                                                                                                                                                     Best Local Similarity 89.5
Matches 17; Conservative
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05-MAR-1992; JP-084531.
05-MAR-1992; JP-084531.
05-MAR-1992; JP-084531.
05-MAR-1992; JP-084531.
P-DSDB; R42839.
P-PSDB; R42839.
DNA having the genetic information of urea amidolyase originated from Saccharomyces yeast - can be used to prepare high purity urea amidolyase by culturing the transformant comprising the DNA claim 1; Page 10-17; J7pp; Japanese.
This sequence encodes a protein which has urea amidolyase (URL)-activity and is derived from yeast. This sequence may be used within a recombinant plasmid for the production of highly pure URL. Sequence 6265 BP; 1873 A; 1156 C; 1361 G; 1875 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.4; DB 1; Length 6265; Pred. No. 9.2; ); Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-1992 (first entry)
Human acetyl choline receptor alpha gene.
hACR-alpha; myasthenia gravis; MG; neuromyopathy; ds.
                                       Urea amidolyase gene.
Urea amidolyase; URL; yeast; recombinant plasmid; ss.
Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/note= "60N inserted as a spacer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag- d
631. 917
/*tag- e
/note- "60N inserted as spacer"
1028. 1200
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/note- "60N inserted as spacer"
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2671. .2994
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**note= "60N inserted as spacer"
2276. .2430
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'note= "60N inserted as
                                                                                 Location/Qualifiers
627. .6134
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/product= URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.0%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           937 TTGCATATGAGCCTTCCA 954
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/*tag= a
346. 3123
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89. 328
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7*tag= /*13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TTACATATGAGCCTTCCA 18
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 17; Conservat
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05-0CT-1983; 186402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J60078996-A.
                      10-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                24-SEP-1993
     249460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intron
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stimulate the production of protective antibodies upon injection into a mammal that would serve to protect the mammal upon challenge with wild type HEV. The proteins can be used for detection and diagnosis of HEV infection. This CDNA was isolated from primates innoculated with stool suspensions obtained from hepatitis E patients. Sequence 7168 BP; 1223 A; 2294 C. 1267
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a //label= ORF-1 (R91813) //label= ORF-1 (R91813) //tans1_except= pos:3739. .3741, aa:Glu //note= "10 bp nucleic acid sequence TGGTNTTYGA as to be inserted between nucleotides 4390. .4391 for numbering to conform to that given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "10 bp nucleic acid sequence TGGTNTTYGA has to be inserted between nucleotides 43910. 4391 for numbering to conform to that given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- ORF-2 (R91814)
/note= "10 bp nucleic acid sequence TGGTNTTYGA
                                                                                                                                                                                    1; Length 7168;
                                                                                                                                                                                                                                                                                                                                                                                                                          25-NOV-1996 (first entry)
Hepatitis E virus strain SAR-55 cDNA (ATCC 75302).
Hepatitis E virus; HFV; SAR-55 strain; enteric transmission;
Structural region; antigen; detection; antibody; vaccine;
immunisation; infection; ss.
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    has to be inserted between nucleotides 4390. 4391 for numbering to conform to that given in the specification.
                                                                                                                                                                                      ВВ
                                                                                                                                                                                  Score 15.8; DE
Pred. No. 19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= ORF-3 (R91815)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                  Query Match 79.0%; Scc
Best Local Similarity 89.5%; Pre
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                2189 TTACATCTGAGCCTTCTAT 2207
                                                                                                                                                                                                                                                                                                                                                                                           T27394 standard; cDNA; 7158
T27394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5137. .7119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5467
                                                                                                                                                                                                                                                              1 TTACATATGAGCCTTCCAT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis E virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9610580-A2.
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PR 11-APR-1997; US-840316.

PR 11-APR-1997; US-8403348.

DR 19-550B; W81519, W81520.

PR 19-550B; W81519, W81520.

PR 19-650B; W81519, W81521.

PR 19-750B; W81519, W81520.

PR 19-750B; W81519, W81520.

PR 19-750B; W81519, W81520.

PR 29-750B; W81519.

PR 20-750B; W81519.

PR 2
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                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis E virus (HEV) polypeptides encoding nucleic acid SAR-55.
Hepatitis E virus; HEV; SAR-55; diagnostic agent; vaccine; antibody;
passive immunisation; ss.
following SDS-PAGE of cell lysates of insect cells infected with a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant expression vectors pPIC9-1779, -1780 and -1781. Sequence 7158 BP; 1221 A; 2293 C; 1864 G; 1780 T;
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                                                                                                                                        Length 7158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .3741, aa:Glu)
.3759, aa:Glu)
.4083, aa:Glu)
.5013, aa:Glu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .5782, aa:Tyr)
                                                                                                                                                                                   Indels
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                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_except= (pos:4081.
/transl_except= (pos:5011.
/product= "ORF-1 protein"
                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_except= (pos:3739.
/transl_except= (pos:3757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_except= (pos:5780.
/product= "ORF-2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                     79.0%; Score 15.8;
89.5%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "ORF-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.0%; Score 15.8;
89.5%; Pred. No. 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                2189 TTACATCTGAGCCTTCTAT 2207
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/*tag= c
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                                                                                                                                                                                                                         1 TTACATATGAGCCTTCCAT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V71604 standard; DNA; 7168
V71604;
                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-1999 (first entry)
                                                                                                                          Query Match
Best Local Similarity 89.59
Watches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis E virus.
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22-OCT-1998.
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V71604
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See also Q59041-Q61440. 92 G; 70 T;

61 C;

123 A;

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coding-region prediction program CRM.
               354 BP;
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               Sequence
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V42902
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                                                                                                                                                                                                                                                                                                      to transcription prods. of genes, useful for tagging genes, mapping chromosomes and tissue typing claim 3; page 86; 199pp; English.

This sequence tepresents an EST (expressed sequence tag) ESTs are markers for human genes actually transcribed in vivo. Unlike the random genomic DNA sequence tagged sites (STSs), ESTs point directly to expressed human genes within a few years at a fraction of the cost of complete genomic sequencing. Using PCR primers (39419-Q39580 (sequences designed from the ESTs) sublocalisation of an EST can be achieved with panels of fragments from specific chromosomes or pools of large genomic clones in analogous manner. This sequence represents EST00020.

Sequence 354 BP; 126 A; 62 C; 90 G; 70 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTS which can be used as markers tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for individual or firensic identification, for mapping locations of disease-associated genes, for identification, for mapping type, and for prepn. of antisense sequences, probes and constructs. EST00020 has an "excellent" coding probability as evaluated using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                            Particular expressed sequence tags from human CDNA - corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-1994 (first entry)
Human brain Expressed Sequence Tag EST00020.
Gene transcription product; genetic markers; tagging; in vivo; transcription; mappling; locations; chromosomes; chromosomal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging of most human genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 354;
                                                                                               Expressed Sequence Tag human gene marker EST00020. expressed sequence tag; human genome project; chromosome; human gene sequencing; PCR mapping; somatic cell hybrids; subjocalisation; gene tagging; tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.0%; Score 15.2; D
85.0%; Pred. No. 29;
ative 0; Mismatches
                                                                                                                                                                                    07-JAN-1993.
19-JUN-1992; U05222.
12-CJUN-1991; US-716831.
12-FEB-1992; US-837195.
(USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-1993; U01294.
12-FEB-1992; US-837195.
(USSH) US DEPT HEALTH & HUMAN SERVICE.
Adams MD, Moreno RF, Venter CJ;
WPI; 93-272882/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 114; 500pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q59055/c
ID Q59055 standard; cDNA; 354 BP.
                                          039643/c
ID 039643 standard; DNA; 354 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TTACATATGAGCCTTCCATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 TTTCACATGAACCTTCCATG 43
                                                                                     20-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 85.Ut
Fac 17; Conservative
                                                                                                                                                                                                                                                                Venter JC;
                                                                                                                                                                                                                                                                            93-036325/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                            Synthetic.
WO9300353-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1993.
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                                                                                                                                                                                                                                                             Adams MD,
                                                                       039643;
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                                                                                                                                                                                                                                                                               WPI;
                            RESULT
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Programminate

Claim 1: Page 220-224; 1409pp; English.

Claim 1: Page 220-224; 1409pp; English.

The present invention describes a computer readable medium which has the present invention describes a computer readable medium which has the nucleotide sequences SEQ ID No: 1 to 391 (V52134 to V5254) recorded to SEQ ID No: 1 to 391. The nucleotide sequences depicted in SEQ ID No: 1 to SEQ ID No: 1 to 391. The nucleotide sequences depicted in SEQ ID No: 1 to SEQ ID No: 1 to 391, where the nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae CC pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae CC by a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO: 1 that hybridise to the target sequence and isolating mena, produced completification primers derived from the members; or (b) isolating mRNA, DNA or CDNA produced from the members; or (b) isolating mRNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide configuration to the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be consed in diagnosis kits and assays, and pharmaceutical commencial manner of the S. pneumoniae genome. Products from the present convention can be used in diagnosis kits and assays, and pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer readable medium with recorded Streptococcus pneumoniae polynucleotide sequences useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae genome fragment SEQ ID NO:11.
Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2365 T;
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          Length 354;
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-1998.
30-CCT-1997; U19588.
31-CCT-1996; US-029960.
(HUMCA-) HUMAN GENOME SCI INC.
BATASH SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M, Kunsch CA, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1863 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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              ;;
              DB
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       76.0%; Score 15.2; I
85.0%; Pred. No. 29;
tive 0; Mismatches
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Mismatches
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                                                                                                                                                        20
                                                                                                                                                                                                                          62 TTTCACATGAACCTTCCATG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1998 (first entry)
Query Match
Best Local Similarity 85.09
Matches 17; Conservative
                                                                                                                                                     1 TTACATATGAGCCTTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TTACATATGAGCCTTCCATG
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae.
WO9818931-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 98-272225/24.
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Search completed: September 18, 1999, 05:27:26
Job time: 1691 sec
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                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                             T04201
                    8888888
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                                                                                                                                                                                                                            Targeting adenovirus to cell-surface protein - using bifunctional
ligand that interacts with adenovirus fibre and cell-surface protein
ligand that interacts with adenovirus fibre and cell-surface protein
Example 1: Page 34: 43pp; French.
Cadenovirus serotype 5, and introduce Ncol and Kpni sites for cloning. It
cadenovirus serotype 5, and introduce Ncol and Kpni sites for cloning. It
cadenovirus serotype 5, and introduce Ncol and Kpni sites for cloning. It
cadenovirus serotype 5, and introduce Ncol and Kpni sites for cloning. It
cadenovirus to cell-surface proteins of serotype C adenoviruses,
and that human fibronectin module III (sic) functions as a co-receptor
or cofacter. The specification describes a method for targeting
or cofacter. The specification describes a method for targeting
coffice adenovirus using a bifunctional ligand. The bifunctional
ligand comprises a portion capable of interacting with the cell surface protein, and
operion capable of interacting with the cell surface protein, and
operion capable of interacting with the cell surface protein, and
copionally a spacer between the first and second portions. The ligand is
cell an infected cell, or a particular cell type bearing a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding plant citrate synthase - used to regulate flower formation, to improve storage of tubers, etc. and to reduce sprouting claim 5; Page 53-56; 87pp; English.

To identify a cDNA from potato which codes for citrate synthase, a cDNA fragment of citrate synthase from Arabidopsis thaliana was firstly amplified using A.thaliana cDNA and oligos T04202 and T04203 which are complementary to the 5' or 3' end of the coding region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
22-OCT-1998 (first entry)
PCR primer used to mutate part of genome of adenovirus serotype 5.
Domain alpha 2; antigen; major histocompatibility complex class I;
MHC-I; primary receptor; serotype C adenovirus; human; fibronectin;
module III; targeting; cell-surface protein; cellular receptor;
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T04199;
25-JAN-1996 (first entry)
Potato citrate synthase cDNA.
Citrate synthase; flower formation; tuber storage; ss.
Solanum tuberosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AGRE ) HOECHST-SCHERING AGREVO GMBH.
La Cognata U, Landschutze V, Muller-rober B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.2;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T04199 standard; cDNA to mRNA; 1891 BP.
                                                                                                                          FR2758822-A1.
31-JUL-1998.
09-SEP-1997; 011166.
30-JAN-1997; FR-001005.
(CNRS ) CNRS CENT NAT RECH SCI.
Boulanger P, Hong SS, Karayan L;
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85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73. .1485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAR-1994; DE-408629.
22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E00859
                                                                                                                                                                                                                    WPI; 98-416459/36.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           La Cognata U, Land
Mueller-roeber B;
WPI; 95-328278/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 BP;
                                                                                                                   Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; R82838
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07-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9524487-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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A. thaliana cDNA for citrate synthase. The oligos additionally introduce BamHI cleavage sites at both ends of the amplified cDNA fragment. a cDNA library was prepd. from potato leaves and screened with A. thaliana citrate synthase cDNA. Positive clones were purified and sequenced. The nt sequence is given in T04199. Sequence 1891 BP; 512 A; 370 C; 425 G; 584 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                DB 1; Length 1891;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 G;
                                                                                                                             Score 14.8; D
Pred. No. 56;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.8; DE
Pred. No. 56;
0; Mismatches
                                                                                                                                                                                                                                                                                          T04201 standard; cDNA to mRNA; 1747 BP T04201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-WAR-1994; DE-408629.
22-SEP-1994; DE-435366.
19-OCT-1994; DE-438821.
(AGRE ) HOECHST-SCHERING AGREVO GMBH.
                                                                                                                                                                                                                                                                                                                        25-JAN-1996 (first entry)
Tobacco cirrate synthase cDNA.
Cirrate synthase; flower formation:
Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                           74.0%;
88.9%;
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88.9%;
                                                                                                                                                                                                       688 ACATATGAGGATTCCATG 705
                                                                                                                                                                                     3 ACATATGAGCCTTCCATG 20
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                                                                                                                                                                                                                                                                                                                                                                                                       70. .1476
/*tag= a
                                                                                                                     Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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07-MAR-1995; E00859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1747 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mueller-roeber B;
WPI; 95-328278/42.
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Matches 16; Conser
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OM nucleic

Run on:

Searched: Database

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(without alignments)
28.079 Million cell updates/sec
                                           ; Search time 1405 Seconds
       Compugen Ltd
GenCore version 4.5
Copyright (c) 1993 - 1998 Comp
                                                                                                                   986266752 residues
                                          September 18, 1999, 06:47:46
                            - nucleic search, using sw model
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20
1 TTACATATGAGCCTTCCATG
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em_est12:*
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em_est19:*
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9b_est6..*
9b_est7..*
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9b_est11..*
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gb_est32:*
em_est20:*
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em_est4:;
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                                                                                                     IDENTITY_NUC
                                                                                                                                   EST: *
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Sequence:
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DEFINITION ACCESSION

NID VERSION

RESULT R19433/c

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H90734 YURRAO4.51
H95824 YV20a11.51
AA17351 WU21606.r
AA2288092 Vb14d09.r
AA377278 ESTB9818
AA377278 ESTB9818
AA370389 VW04a06.r
AA70389 VW04a06.r
AA65383 Vx15d05.r
AA18550 Uy73a08.r
AA18579 Yq53h03.r1
H7857 YU99e01.r1
AA40116 ZUS10768
H08527 Y189a12.r1
H4725 YMA4C02.r1
R61347 Y18469.s1
H82720 YV27401.r1
N46516 Y942701.r1
AA280522 ZU10b12.r
AA280522 ZU10b12.r
AA270555 Va66h11.r
AA280446 Vb18b04.r
AA379224 EST92062
AA444013 ZW25901.r
                                                                       R19433 y925c03.r1
D55860 HUM404C08B
N29325 yw84c11.s1
AA831249 oc73e01.s
AA908884 om51f02.s
AI130847 qc14a10.x
AI248140 qh75b12.x
D52258 HUM072G05B
                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                               yg25c03.rl Soares infant brain lNIB Homo sapiens cDNA clone IMAGE 33575 5', mRNA sequence. R19433 g773043 R19433.1 GI:7770.
                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                SUMMARIES
                                                                       R19433
D55860
AA90325
AA9081249
AA9081249
AI130847
AI248140
D52258
D52258
H90734
H90734
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AA863883
AI226166
R93797
H78857
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AA275311
AA288092
AA377278
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AA748850
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R6547
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        Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takalohi,A., Takeda,S., Natanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
Fujiwara et al. (1995)
Unpublished (1995)
on Sep 21, 1992 this sequence version replaced gi:279304.
                                                                                                                                           Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, 771-01 Japan
Fax: 0886-65-2888
Fax: 0886-57-1035
Fax: 0886-65-2888
Insert Length: 802 Std Error: 0.00
High quality sequence stop: 353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yw84c11.sl Soares_placenta_8to9weeks_2NbHP8tc99W Homo sapiens cDNA clone IMAGE:258932 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stops: 278
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 278.
Location/qualifiers
1. -476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 476)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Hultman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaski, E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GEN-404C08"
/clone="jib="Clontech human fetal brain polyA+ mRNA (#6535)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
On May 18, 1995 this sequence version replaced gi:810971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23;
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Pred. No. 36;
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90.0%;
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N29325.1 GI:1147845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                       source
                                                                           TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
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SOURCE
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                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 40; N.) Dubuque, T., Elliston, K., Hawkins, M.,
Hillier, L., Clark, N., Dubuque, T., Eliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D55860 360 bp mRNA EST 31-AUG-1995
HUM404C08B Clontech human fetal brain polyA+ mRNA (#6535) Homo
sapiens cDNA clone GEN-404C08 5', mRNA sequence.
D55860
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 360)
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/clone_lib="Soares infant brain lNIB"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.0%; Score 17.4; DB 21;
94.7%; Pred. No. 17;
ive 0; Mismatches 1;
                                                                                                                                                                                    The WashU-Merck EST Project
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D55860.1 GI:970260
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                                                                                                                                                                                                        Unpublished (1995)
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Best Local Similarity 94.7
Matches 18; Conservative
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Final: Robert_Strausbergenih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-GGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (Dases 1 to 493)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                            constructed by Bento Soares and M. Fatima Bonaldo."
94 c 69 q 142 t
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/clone_lib="NCI_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_bost="DH108"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                        84.0%; Score 16.8; DB 39; 90.0%; Pred. No. 36;
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High quality sequence stop: 467.
Location/Qualifiers
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/db_xref="taxon:9606"
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AA908884.1 GI:3048289
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Unpublished (1997)
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Best Local Similarity
Matches 18; Conserv
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                           Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1550
Email: Robert_Strausberg@inh.gov
Tissue Procur_Strausberg@inh.gov
Ph.D., Gerald Marti, M.D.
ConM. Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2285618.
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Pred. No. 36;
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:1353352"
/clone_lib="NCI_CGAP_GCB1"
/organism="Homo sapiens"
/db_xref="GDB:3888638"
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AA831249.1 GI:2904348
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90.0%;
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                                                                                                                                                                                                                                                                                                                                               AI130847 598 bp mRNA EST 27-OCT-1998 qc14a10.xl Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone IMAGE:1709562 3' similar to SW:YN8H_YEAST P53729 HYPOTHETICAL 48.1
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 598)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.linl.gov) for further information.
Insert Length: 771 Std Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 440.
Location/Qualifiers
1.598
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On Jan 9, 1998 this sequence version replaced gi:930548.
                                                                                                                                                                              Length 493;
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/db_xref="taxon:9606"
/clone="IMAGE:1709562"
/clone_lib="Soares_fetal_heart_NDHH19W"
/sex="unknown"
                                                                                                                                                                              DB 40;
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                                                                                                                                                                           84.0%; Score 16.8; 1
90.0%; Pred. No. 36;
live 0; Mismatches
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AI130847.1 GI:3600863
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Best Local Similarity 90.0
Matches 18; Conservative
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A1248140 567 bp mRNA EST 01-DEC-1998 qh/5b12.xl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:1850495 3' similar to SW:YN8H_YEAST P53729 HYPOTHETICAL 48.1 KD PROTEIN IN SEC12-SSK2 INTERGENIC REGION. ;, mRNA sequence.
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 772 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 354.
Location/Qualifiers
1. 567
/organism="Homo sapiens"
/db_xref="tamo: 9606"
/map="16pl3:3"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 567)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                         Gaps
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2151692.
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/sex="male"
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0
     Length 598;
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     DB 42;
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Pred. No. 36;
0; Mismatches
                                   0; Mismatches
   Score 16.8;
Pred. No. 37;
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 84.0%;
90.0%;
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                                                                     1 TTACATATGAGCCTTCCATG 20
                                                                                       80 TTACATATGAGACTTTCATG 99
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90.0%;
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Query Match
Best Local Similarity 90.0
Matches 18; Conservative
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Best Local Similarity
Thes 18; Conserve
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313 TTACATATGAGACTKTCATG 294
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85.0%;
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H90734.1 GI:1081164
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Very vara T., Hirano, H., Kategizi, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Fujiwara et al. (1995)

Unpublished (1995)
                                                                                                                                                                             Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharyota; Primates: Catarrhini; Hominidae; Homo.

1 (bases 1 to 379)
1 (bases 1, 0 379)
1 (bases 1, 0 379)
2 (bulyuara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Ckuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Fujiwara et al. (1995)
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                 Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-52-288
Fax: 0886-37-1035
Insert Length: 572 Std Error: 0.00
                                   D52258 379 bp mRNA EST 14-SEP-1995
HUM072G05B Clontech human fetal brain polyA+ mRNA (#6535) Homo
sapiens cDNA clone GEN-072G05 5', mRNA sequence.
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HUM106D02B Clontech human fetal brain polyA+ mRNA (#6535) Homo
sapiens cDNA clone GEN-106D02 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini: Eominidae; Homo.
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/db_xref="taxon.9606"
/clone="GEN-072605"
/clone="Lib="Clontech human fetal brain polyA+ mRNA (#6535)"
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85.0%; Pred. No. 58;
:ive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tsutomu Fujiwara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Isutomu Fujiwara
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D52258.1 GI:952494
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D53341.1 GI:955238
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Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                                  human.
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D52258/c
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yu84a04.sl Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:240462 3' similar to contains Alu repetitive element;, mRNA
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
643-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
Washington University School of Medicine
444 Forset Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Final: est(watson wustl.edu
Insert Size: 809
High quality sequence stops: 369
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@inage.llnl.gov) for further information.
Insert Length: 809 Std Error: 0.00
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
Hillier, Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba;T., Le,M., Lenon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                        1. .402

/doganism="Homo sapiens"

/db_xref="taxon-9606"

/clone="GEN-106002"

/clone="GEN-106002"

/clone="ib="Clontech human fetal brain polyA+ mRNA

(#5535)" 67 9 164 t 3 others
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The WashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:838025.
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/db_xref="GDB:3789595"
/db_xref="taxon:9606"
/clone="IMAGE:240462"
/clone="lib="soares fetal liver spleen INFLS"
/sex="male"
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Pred. No. 59;
1; Mismatches
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High quality sequence stop: 369.
Location/Qualifiers
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Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                             Query Match
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/dev_arge="10 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; vector: pT7T3D (Pharmacia)
with a modified polylinker; Site=1: Pac I; Site=2: Eco RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
[5/ AACTGGAAGTAATTATATTTTTTTTTTTTTTTTTTT
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
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Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4414 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality, sequence stops: 315
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward.
                                                                                                                                                                                                                                                                                                 Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Leh., Lennon,G., Marra,M.,
Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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On Jan 25, 1995 this sequence version replaced gi:637882.
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0
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Pred. No. 1.2e+02;
); Mismatches 2; Indels 0
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/db_xref="taxon:9606"
/clone="IMAGE:243260"
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IMAGE:243260 3', mRNA sequence.
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89.5%;
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Matches 17; Conservative
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and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo." 87 c 94 g 117 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washigton University School of MedicineP
Washigton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                          AA197351 630 bp mRNA EST 19-FEB-1997 mu21e06.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:640066 5'
                                                                                                                                                                                                                     Gaps
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On Sep 12, 1996 this sequence version replaced gi:1393441
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0
                                                                                                                                                                  Length 424;
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                                                                                                                                                             79.0%; Score 15.8; DB 24;
89.5%; Pred. No. 1.2e+02;
ive 0; Mismatches 2;
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Location/Qualifiers
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/clone="IMAGE:640066"
/clone_lib="Soares 2NbMT"
/sex="male"
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/organism="Mus musculus"
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/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA197351.1 GI:1792993
                                                                                                                                                                                                                                                                                       296 TACATTTGAGGCTTCCATG 278
                                                                                                                                                                                                                                                         2 TACATATGAGCCTTCCATG 20
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427;

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79.0%;
89.5%;
                                                                                                           19 TAGATCTGAGCCTTCCATG 37
                                                                                       2 TACATATGAGCCTTCCATG 20
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87 c
       Query Match 79.U1
Best Local Similarity 89.51
Matches 17; Conservative
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Best Local Simi
Matches 17;
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                                                                                                                                                                                     RESULT 14
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lymph node; Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wilson,R. and
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vc06a11.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone
IMAGE:765692 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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On Nov 29, 1993 this sequence version replaced gi:430191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                         ö
                                               Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/organism="C57BL/6J"
/db.xref="Laxon:10090"
/clone="IMAGE:765692"
/clone=lib="Soares mouse lymph node NbMLN"
/sex="male"
                                                                                         Indels
                                               Score 15.8; DB 30;
Pred. No. 1.2e+02;
0; Mismatches 2;
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Seg primer: -28ml3 rev2 Er from Amersham
High quality sequence stop: 406.
Location/Qualifiers
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/dev_stage="4 weeks"
/lab_host="DH10B"
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The WashU-HHMI Mouse EST Project
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AA275311.1 GI:1915708
                                                   79.0%;
89.5%;
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                                                                                                                               2 TACATATGAGCCTTCCATG 20
                                         Query Match
Best Local Similarity 89.59
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
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ORIGIN
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AUTHORS
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LOCUS
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SOURCE
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ORIGIN
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 432)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Wnorris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
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                                                                                                                                                                                                                                                AA288092 432 bp mRNA EST 11.APR-11997 vb14009.r1 Scares mouse NML Mus musculus cDNA clone IMAGE:748913 5′, mRNA sequence.
AA288092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:457897
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                                                Gaps
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Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1397406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
Washu-HHh <sup>T</sup> Mouse EST Project
Washingtc. University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels 0
  Length
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 406.
Location/Qualifiers
Location/Qualifiers
Location/Qualifiers
Assarian musculus"
Ab_xref="taxon:10090"
Aclone="InAGE: AB913"
Aclone="InAGE: AB913"
Atissue_type="Liver"
Atissue_type="Liver"
Anabost="MH10B"
Score 15.8; DB 31;
Pred. No. 1.2e+02;
0; Mismatches 2;
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89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TACATATGAGCCTTCCATG 20
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                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 372)
Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C. Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library
Nature Genet. 4, 373-380 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers

1. 372
Aorganism="Homo sapiens"
Ab_xref="AACC (inhost):181679"
Ab_xref="AACC (inhost):181679"
Abox ref="AACO:9606"
Aclone_lib="Small intestine II"
Adev_stage="adult"
Anotes"Organ: small intestine; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
a 68 c 72 g 114 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                        AA377278 372 bp mRNA EST 21-APR-1997
EST89818 Small intestine II Homo sapiens CDNA 3' end, mRNA
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0
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                                                           sequence.
AA377278
92029596
AA377278.1 GI:2029596
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human.
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VERSION
KEYWORDS
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RESULT 15
AA377278/C
                             LOCUS
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AUTHORS
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Search completed: September 18, 1999, 06:47:49 Job time: 3666 sec

us-09-037-472-7.rst

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/organism="Zea mays"

/organism="Tea" on the state of the stat
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/organism="Drosophila melanogaster"
/db_xref="BDGP_EST:BDcln008999"
/db_xref="taxon:7227"
/clone="LD09712"
/clone_lib="LD Drosophila melanogaster embryo BlueScript"
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LD09712.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD09712 5prime, mRNA sequence.
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University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Exa: 510 643 9947
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 97 row: A column: 12
High quality sequence stop: 458.
Location/Qualifiers
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Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 466)
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On Sep 12, 1996 this sequence version replaced gi:1406966.
University
Unpublished (1999)
On Jul 28, 1997 this sequence version replaced gi:2065396.
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                                                                                                                                                                                 Department of Biological Sciences Stanford University Tel: 620 1/50 123 227 Fax: 650 723 222 Email: walbockstanford.edu Fax: 650725 822 Email: walbockstanford.edu Plate: 605055 row: 6 column: 07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.6%; Score 16.2; DB 50;
85.7%; Pred. No. 2e+02;
iive 0; Mismatches 3;
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AA390812.1 GI:2043958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.6
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                     Contact: Walbot V
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/sex="male and female"
//sex="male and female"
//sex="male and female"
//lab_host="Solm"
//lab_host="Solm"
//lab_host="Solm"
//lab_host="Solm"
//solm: Sine_2: XhoI: Constructed using Stratagene ZAP-CDNA
Synthesis kit. Oligo dT-primed and directionally cloned at
Synthesis kit. Oligo dT-primed and directionally cloned at
ONIGIN

Query Match
72.7%; Score 16; DB 33; Length 466;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 GTTCTACCACCTGAAC 17
Db 77 GTTCTACCACCTGAAC 92
Search completed: September 18, 1999, 06:47:46
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LOCUS

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A1677476 603 bp mRNA EST 25-MAY-1999
605055G07.x1 605 - Endosperm cDNA library from Schmidt Lab Zea mays
CDNA, mRNA sequence.
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/clone_lib="603 - stressed root cDNA library from
wang/Bohnert lab"
/tissue_type="seedling"
/dev_steg_type="sell stress"
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/note="organ: root cDNA library from Wang/Bohnert lab"
a 186 c 118 g 143 t
                                                                   603001C11.X1 603 - stressed root cDNA library from Wang/Bohnert lab Zea mays cDNA, mRNA sequence.
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euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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euphyllophytes, Spermatophyta, Magnoliophyta, Liliopsida, Poales;
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Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 620)
Walbot,V
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact. Mails of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 723 227
Fax: 650 725 8221
Email: walbockestanford.edu
Plate: 603001 row: C column: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.6%; Score 16.2; DB 49;
85.7%; Pred. No. 2.1e+02;
ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"/cultivar="B73"
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Best Local Similarity 85.7%
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Walbot V
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FORMARD: EXI (5'-CGACGACGACGACGAGGCCA-3')
BACKWARD: HIS1 (5'-GTAGTGGTGGTGGTGGTG-3')
Plate: MEST1 row: D column: 3
Seq primer: POLYT-N (5'-TITITITITITITITITITITITITIAGC)-3')17-1.
                                                                                                                                                                                                                         AI374544 909 bp mRNA EST 21-JAN-1999 MEST1-D3.POLYIN.Seq ISUM1 Zea mays cDNA clone MEST1-D3 5', mRNA
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On Jan 17, 1998 this sequence version replaced gi:1900949
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    Length 452;
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/dev_stage="two-week-old green seedling"
/lab_host="BL21(DE3)"
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 909)
Wen,T.J., Ashlock,D.A. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings
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85.7%; Pred. No. 2.2e+02;
live 0; Mismatches 3;
73.6%; Score 16.2; DB 38;
85.7%; Pred. No. 1.9e+02;
ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G405 Agronomy, Ames, IA 50011, USA
Tel: (515)-294-0975
Fax: (515)-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref-"taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: schnable@lastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="MEST1-D3"
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                                                                                                      408 TGTTCTACCACCTGTGCTATG 388
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                                                                                 1 TGTTCTACCACCTGAACTAGG 21
                                                                                                                                                                                                                                                                                                                            GI:4174564
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Schnable laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iowa State University
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Matches 18; Conservative
                                         18; Conservative
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AI374544.1
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2 GITCIACCACCIGAACTAGGC
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                   AA063903 524 bp mRNA EST 03-FEB-1997 m140al0.rl Stratagene mouse testis (#937308) Mus musculus cDNA clone IMAGE:514458 5' similar to 9b:M1560 FRUCTOSE-BISPHOSPHATE ALDOLASE A (HUMAN); 9b:Y00516 Mouse mRNA for aldolase A (MOUSE);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
/db_xref="taxon:6239"
/clone="yk8549"
/clone=lib="Yuji Kohara unpublished cDNA"
/note="dev_stage=varied, sex=Hermaphrodite male, tissue_type=whole animal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fas: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
On May 5, 1995 this sequence version replaced gi:798078
                                                                                                                                                     Score 16.2; DB 24; Length 360; Pred. No. 1.8e+02; 0; Mismatches 3; Indels 0
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Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 59.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
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Best Local Similarity 85.7%;
Matches 18; Conservative
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                               ö
                                                                                                                                                                                                                                              AA808387 452 bp mRNA EST 12-FEB-1998 oa90d09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1319537 3's similar to TR:Q06265 Q06265 AUTOANTIGEN PM-SCL. [1]; , mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 452) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Jan 19, 1998 this sequence version replaced gi:2153347
                                               ..
0
  Length 524;
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1319537"
/clone=lib="NCI_CGAP_GCBI"
/tissue_type="germinal center B cell"
/lab_host="DH108"
  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seg primer: -40ml3 fwd. ET from Amersham
Score 16.2; DB ;
Pred. No. 2e+02;
                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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                                                                                                            192 GTACTACCACCGGAACTATGC 212
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D74792 360 bp mRNA EST 14-DEC-1995 CELK085D9F Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA clone yk85d9 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis clegams.

Eukaryota; Metascoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis:

1 (bases 1 to 360)

(bases 1 to 360)

Tabara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and Tabara, H.
                                  High qality sequence stops: 282 Source: IMAGE Consortium, LLNL Th clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
Insert Length: 978 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toward an expression map of the C.elegans genome Unpublished (1994)
On Sep 21, 1992 this sequence version replaced gi:276019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 380;
                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:127624"
/clone_lib="Soares fetal liver spleen INFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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/strain="CB1489 him-8(e1489)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.6%; Score 16.2; DB 21;
85.7%; Pred. No. 1.9e+02;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 0559-75-0771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 0559-75-6240
Email: ykohara@ddbj.nig.ac.j
Insert Length: 1084 Std Error: 0.00
High quality sequence stop: 1.
                                                                                                                                                                                       1. .380
/organism="Homo sapiens"
                                                                                                                                                                                                                                  /db_xref="GDB:479785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
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                  Insert Size: 978
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JOURNAL
COMMENT
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KEYWORDS
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D74792/c
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                                                                                                                                                                 CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R09403 380 bp mRNA EST 05-APR-1995 yf22e09.rl Soares fetal liver spleen lNFLS Homo sapiens CDNA clone IMAGE:127624 5', mRNA sequence.
           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 380; Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Socres,M., Tan,F., Treyaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled germ cell tumors"
//lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.8; DB 49;
Pred. No. 93;
0; Mismatches 2;
                                                                                                                                                                                                                                                       www-bio.llnj.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:2306208"
/clone_lib="NCI_CGAP_GC6"
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                  Seq primer: -40UP from Gibco
High quality sequence stop: 363.
Location/Qualifiers
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R09403.1 GI:761326
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Best Local Similarity 90.0 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1995)
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JOURNAL
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AUTHORS
TITLE
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A1652206
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(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTITITITITITITITI]; double-strand cDNA was
ligated to a DraIII adaptor [TGTTGGCTAATGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTTGGTCTAAAAGCTGGG and 3' end
primer CGACCTGCAGCTCGAGCACA."

53 a 138 c 161 g 157 t.
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5' similar to WP:T08G11.4 CE13449 ;, mRNA sequence.
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The Washu-NOI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Mammalia;
Eutheria: Rodentia: Sclurognathi; Muridae: Murinae: Mus.
1 (bases Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                    On May 18, 1998 this sequence version replaced gi:3138157
                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.4%; Score 16.8; DB 47: Length 709; 90.0%; Pred. No. 1.1e+02; Live 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                      Possible reversed clone: similarity on wrong strand Seq primer: custom primer used High quality sequence stop: 510.

Location/Qualifiers
                                                                                                                                                                                Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:1922530"
/clone_lib="Sugano mouse kidney mkia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/map="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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Best Local Similarity
Matches 18; Conserv
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JOURNAL
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3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M. Patima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TT-01: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, R.
The Wash J. NCI Mouse EST Project 1999
Unpublished (1999)
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Eukaryota: Metazoa: Chordata; Craniata: Vertebrata: Mammalia:
Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 376)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                              On May 7, 1998 this sequence version replaced gi:3121071.
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Unpublished (1997)
On May 7, 1998 this sequence version replaced gi:3121284
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/clone="IMAGE:617668"
/clone=lib="Soares mouse 3NbMS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.4%; Score 16.8; D
90.0%; Pred. No. 98;
iive 0; Mismatches
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Seg primer: -40RP from Gibco
High quality sequence stop: 476.
Location/Qualifiers
1. .484
/organism-"Mus musculus"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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AI652206.1 GI:4736185
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Mon

ORGANISM

REFERENCE

VERSION KEYWORDS SOURCE

ACCESSION

TITLE

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/note="Vector: pBl:norript SK; Site_1: Sall; Site_2: NotI; Cambial region tiscuse, including developing xylem, the meristematic cambial zone and the developing and mature pholom, was harvested from 1.5 m actively growing trees. CDNA was prepared and cloned into lambda gt22a. DNA was isolated and subcloned into pBluescript SK using Sall and NotI restriction 119 t 5 others
                                                                                                                                                                                                                   Sterky, F., Regan, S., Karlsson, J., Hertzberg, M., Rohde, A., Holmberg, A., Amini, B., Bhalerao, R., Larsson, M., Villarroel, R., Van Montagu, M., Sandberg, G., Olsson, O., Teeri, T.T., Boerjan, W., Gustafsson, P., Uhlen, M., Sundberg, B. and Lundeberg, J. Gene discovery in the wood-forming tissues of poplar: Analysis of 5,692 expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
                                                    Populus tremula x Populus tremuloides.
Populus tremula x Populus tremiloides
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 465)
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uj41e06.yl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:1922530 5' similar to WP:T08G11.4 CE13449 ;, mRNA sequence.
AIS26675
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases I to 709)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Populus tremula x Populus tremuloides"
/db_xref="taxon:4765;"
/clone_lib="Hybrid aspen plasmid library"
/tissue_type="Cambia! region"
/dev_stage="l.5 m actively growing tree"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                       On Jan 9, 1998 this sequence version replaced gi:930585.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Sterky F
Department of Bi technology
Royal Institute of Technology (KTH)
Teknikringen 34, S-100 44 STOCKHOLM, Sweden
Tel: +46 8 790 8287
Fax: +46 8 24 54 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.4%; Score 16.8; DB 43; 90.0%; Pred. No. 97;
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0; Mismatches
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Seq primer: CGTTGTAAAAGAGGGGCGCAG
High quality sequence stop: 465.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: fredrik@biochem.kth.se
PCR PRimers
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        AI161663.1 GI:3852948
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Best Local Similarity 90.0
Matches 18; Conservative
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fetlina Bonaldo."
                                                                                                                                                                                                                                    1 (bases 1 to 482)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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A004P75U Hybrid aspen plasmid library Populus tremula x Populus
tremuloides CDNA 5', mRNA sequence.
Ali61663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:378492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1288871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.4%; Score 16.8; DB 29; Length 482; 90.0%; Pred. No. 98; tive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares mouse 3NbMS" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: -28Ml3 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 455.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/map="1q"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Spleen"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:617668"
;, mRNA sequence
                                                                           AA174934.1 GI:1756082
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                                                                                                                                house mouse.
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source

FEATURES

ô

Gaps

; 0

Query Match

Matches

BASE COUNT ORIGIN

RESULT 4 A1161663/c

DEFINITION

LOCUS

ACCESSION

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Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Info@egenomesystems.com) and Research Genetics, Huntsville. Alabama
(web address: www.resgen.com) (email contact: info@esogen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA174934 482 bp mRNA EST 16-FEB-1997 ms78c03.rl Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:517668 5' similar to TR:E246895 E246895 CHROMOSOME XVI READING FRAME ORF
                        l (bases 1 to 238)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M.,
Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Wasturston, R. and Wilson, R.
Washy Zebrafish EST Project 1998
Unpublished (1998)
On Jun 5, 1998 this sequence version replaced gi:3188593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="zebrafish WashU MPIMG EST"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 48;
             Cyprinoidea; Cyprinidae; Rasborinae; Danio
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Pred. No. 53;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 106.
Location/Qualifiers
1. .238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www.rzpd.de)
Seq primer: T3 ET from Amersham
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                                                                                                                                                                                                                                                                      Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 TGCTCTACAAGCTGAACTAGGC 204
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86.4%;
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                                                                                                                                                                                 TITLE
JOURNAL
                                 REFERENCE
                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
AA174934
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1558929 238 bp mRNA EST 24-MAR-1999 fb78b02.yl Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to WP:T04C9.6 CE04881 BAND 4.1-LIKE DOMAIN ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I: Site_2: Eco RI: 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 443)
NCI.CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                       Tel: (301) 496-1550
mail: Robert_Strausberg@nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                      On Sep 12, 1996 this sequence version replaced gi:1398118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Possible reversed clone: similarity on wrong strand Insert Length: 1127 Std Error: 0.00 Seq primer: -40ml3 Hwd. ET from Amersham High quality sequence stop: 76. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.2%; Score 17.2; DB 39; Best Local Similarity 86.4%; Pred. No. 60; Matches 19; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1409081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host-"DH10B"
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  AA860156.1 GI:2954151
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Unpublished (1997)
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                                                                 Homo sapiens
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VERSION
KEYWORDS
SOURCE
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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nucleic search, using sw model OM nucleic

September 18, 1999, 06:47:43; Search time 1405 Seconds (without alignments) 30.887 Million cell updates/sec

Run on:

2546578 seqs, 986266752 residues 1 TGTTCTACCACCTGAACTAGGC 22 US-09-037-472-7 IDENTITY\_NUC EST: \* Title: Perfect score: Scoring table: Database : Sequence: Searched:

em\_est22:\*
em\_est23:\*
em\_est24:\*
em\_est25:\*
em\_est25:\* 554 ... 57 ... 58 ...

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

6 ak47b09.	4 ms/8c03. 3 A004P75U 5 uj41e06. 5 ms78c03.	<pre>/6 wb20c01. yf22e09.r1 CELK085D9F // m140a10.</pre>	7 MEST1-D3 4 MEST1-D3 9 603001C1 6 605055G0 2 LD09712. 6 LD16566.	6 LD30041. 3 vi69904. 5 op80011. 8 AU033738. 3 AU033743 9 AU000589	M LD40035. Y211a06.s1 K3598F Hum ma92b05.r1 mb90909.r1 zd51b11.r1	0 mg81b mf94902 mf94902 zf72d c mj99b 0 ze88h 0 ze88h mp05e 1 mm02e 8 zq40e 8 zq40e 0 mx149
36015 55892	166	9230	338 338 338 338 747 747 747	3373 3374 3374 3374 3374 3374 3374 3058	071 071 071 002 002	471100000000000000000000000000000000000
39	443	24 24 28	8 4 4 5 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	50 50 50 50 50 50 50 50 50 50 50 50 50 5	22 22 22 23 23 33 33
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	η 14 πν Φ L	00 10 10	c 11 c 12 c 13 c 14 15	C 118 22 23 24 23 24 25 25 25 25 25 25 25 25 25 25 25 25 25	C C C C C C C C C C C C C C C C C C C	0000 00 00 00 00 00 00 00 00 00 00 00 0
	1 17.2 78.2 443 39 AA860156 AA860156 ak47b09.2 17.2 78.2 238 48 AI558929 A1558929 ED78b02.3 16.8 76.4 49.5 50.5 50.5 50.5 50.5 50.5 50.5 50.5 5	1 17.2 78.2 443 39 AA860156 AA860156 ak47b09.2 17.2 78.2 238 48 A1558929 A1558929 fb7bb02.3 16.8 76.4 482 29 AA174934 AA17803755 A1558675 A1539755 MA186063.3 MA186063 AA18639755 MA186063.3	17.2 78.2 443 39 AA860156 AA860156 AA860156 AA75099.2 17.2 78.2 238 48 AA158929 AA558929 AA558929 Fb78b02.3 16.8 76.4 462 29 AA144934 AA174934 MA78e03.5 16.8 76.4 709 47 AI5526675 AA156675 AA15606.5 16.8 76.4 49 A1659755 A1652206 WA20001.5 16.8 76.4 49 A1652206 A1652206 WA20001.5 16.8 76.4 376 49 A1652206 A1652206 WA20001.5 16.8 76.4 376 49 A1652206 A1652206 WA20001.5 16.8 76.4 376 49 A1652206 A1652206 WA20001.5 16.2 73.6 380 24 D74792 CELKOBSDEF.	17.2 78.2 433 9 AA860156 AA860156 AA756095 EA756095 17.2 78.2 438 48 A1558929 A756095 47.5 78.2 438 48 A1558929 A756095 47.5 78.2 48.2 29 AA174934 AA1756675 AA1639755 M56095 A1639755 M56095 A163975 M56095 A1637149 A1637	1 17.2 78.2 28.8 AA860156 AI558929 fb7bb09. 2 17.2 78.2 28.8 48 AI558929 AI568029 fb7bb09. 3 16.8 76.4 482 29 AA174934 AA174934 AA174934 MS7B603. 4 16.8 76.4 484 49 AI568025 AI6683 A0478203. 6 16.8 76.4 484 49 AI659755 AI658206 Wa20001. 8 16.2 73.6 340 AI652206 AA680387 AI658206 Wa20001. 10 16.2 73.6 524 BA4080387 AA808387 CELK085D9F. 11 16.2 73.6 524 BA4080383 AA808387 CELK085D9F. 12 16.2 73.6 524 AA808387 AA808387 CELK085D9F. 13 16.2 73.6 620 49 AI637149 AA808387 CELK085D9F. 14 16.2 73.6 620 49 AI637149 AA808387 CELK085D9F. 15 16.2 73.6 620 49 AI637149 AA808387 CELK085D6F. 16 72.7 466 33 AA30812 AA90812 LD09712. 16 72.7 466 33 AA30812 AA90812 LD09712. 18 15.8 71.8 488 40 AA971375 AA9803138 AU033738 AU033738 AU033738 AU033738 AU033738 AU033738 AU033738 AU033738 AU033738 AU006589 AU0000589 AU0000589 AU0000589 AU006587 AU004377 A	17.2

em\_est16:\*
em\_est17:\*
em\_est17:\*
em\_est17:\*
em\_est19:\*
ep\_est2:\*
ep\_est4:\*
ep\_est4:\*
ep\_est4:\*
ep\_est6:\*
ep\_est6:\*
ep\_est17:\*
ep\_est112:\*
ep\_est112:\*
ep\_est12:\*
ep\_est12:\*

em\_est10:\*
em\_est11:\*
em\_est12:\*
em\_est13:\*
em\_est14:\*

em\_est1:...
em\_est2:...
em\_est4:...
em\_est5:...
em\_est5:...
em\_est7:...
em\_est8:...
em\_est8:...

ALIGNMENTS

90-est15::990-est15::990-est15::990-est17::990-est19::990-est29::9

gb\_est31:
gb\_est32:
em\_est20:
em\_est21:

AA860156 443 bp mRNA EST 04-JAN-1999 ak47b09.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1409081 3' similar to SW:RSU1\_HUMAN 015404 RAS SUPPRESSOR PROTEIN 1 ;, mRNA sequence.
AA860156 RESULT 1 AA860156/c LOCUS DEFINITION ACCESSION NID

9

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The present invention describes a computer readable medium which has the present invention describes a computer readable medium which has the present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The nucleotide sequences from Streptococcus consuments of the present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genome (SEQ ID NO:1 that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or CDNA produced from the members; or (b) isolating mRNA, DNA or CDNA produced sequence is homologues to amplification primers derived from the cragment of the S. pneumoniae genome to prime the amplification and computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present compositions and vaccines for S. Dneumoniae genome. Products from the present compositions and vaccines for S. Dneumoniae genome. Products from the present compositions and vaccines for S. Dneumoniae genome. Products from the present compositions and vaccines for S. Dneumoniae genome. Products from the present compositions and vaccines for S. Dneumoniae genome. Products from the present compositions and vaccines for S. Dneumoniae genome. Products from the present compositions and vaccines for S. Dneumoniae genome. Products from the present compositions and vaccines for S. Dneumoniae genome. Products from the present compositions and vaccines for S. Dneumoniae genome. Products from the present compositions and vaccines for S. Dneumoniae genome. Products from the present compositions and vaccines f
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                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 98-27225/24. Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae genome fragment SEO ID NO:198.
Streptococcus pneumoniae: S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                      ö
                                                                                     Length 335;
                                                                                                                                      4; Indels
            79 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-0CT-1997; U19588.
31-0CT-1996; US-029960.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M,
                                                                                     DB 1;
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          94
                                                                                                                              0; Mismatches
                                                                                Score 15.6; |
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
       68 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae
Claim 1, Page 1169-1173; 1409pp;
                                                                                                                                                                                                    206 TGCTCTACCAACTGAGCTATGC 185
                                                                                                                                                                       1 TGTTCTACCACCTGAACTAGGC 22
                                                                                                                                                                                                                                                                                                                                             V52331 standard; DNA; 6846 BP.
                                                                             70.9%;
81.8%;
     94 A;
                                                              Query Match
Best Local Similarity 81.8#
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ereptococcus pneumoniae WO3818931-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
  335 BP;
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Sequence
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Query Match

Query Match

Best Local Similarity 81.8%; Pred. No. 74;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 TGTTCTACCACCTGAACTAGGC 22
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Search completed: September 18, 1999, 05:27:24 Job time: 1689 sec

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q14103/c
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derived from spacer region between 16S and 23S rRNA genes, for
detecting e.g. BORDETELLA PERTUSSIS, NEISSERIA GONORRHOEAE
Disclosure: Fig 3: 41pp: English.
This sequence is the non-coding strand of the 16S-23S rRNA gene
spacer region: the 5-end is proximal to the 16S rRNA gene and the 3'-end proximal to the 23S rRNA gene. The sequence is very similar
to the corresponding region in Ngonorrhoeae ITM 4367. A set of
probes was designed based on this sequence which was specific for
N.gonorrhoeae. A kit is provided for detection of N.gonorrhoeae
engange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
20-JAN-1993 (first entry)
Encodes exons XV to XVII of human hepatocyte growth factor.
HGF: enhance growth: preparing transgenic animals; hepatic disease;
Clinical diagnostic reagent; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 22; 28pp; Japanese.
This sequence contains exons XV to XVIII of human hepatocyte growth factor. See also R25676-92, Q26713-27.
Sequence 7753 BP; 2567 A; 1177 C; 1243 G; 2766 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.gonorrhoeae strain NCTC 8375 16S to 23S rRNA gene spacer region.
TRNA gene: ribosomal RNA; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant human hepatocyte growth factor and DNA encoding it useful for diagnosis and treatment of hepatic disease and transgenic animal prepr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
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71.8%; Score 15.8;
Best Local Similarity 89.5%; Pred. No. 60
Matches 17; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          991. .1136

/*tag= c

/note= "exon XVII"

3764. .3937

/*tag= d

/note= "exon XVIII"

7492. .7497
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       /*tag= a /note= "exon XV" 773. 879 /*tag= b /note= "exon XVI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrhoeae NCTC 8375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6269 TGTTCTACCACCTAAAATA 6251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q14102 standard; DNA; 603 BP.
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WPI; 91-311940/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGTTCTACCACCTGAACTA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INNO-) INNOGENETICS NV SA
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19-NOV-1990; 314548.
19-NOV-1990; JP-314548.
(NAKA/) NAKAWURA T.
(TOYM) TOYOBO KK.
WPI; 92-265591/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-1990; 401054.
18-APR-1990; EP-401054.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; R25692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polya_siqual
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DD O1411
DD 
                                                                   NAME OF THE STATE 
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19 23-CT-1991.

19 R 18 - APR-1990; 401054.

19 R 18 - APR-1990; ED-401054.

19 R 18 - APR-1990; ED-401054.

21 CINNO-) INNOGENETICS NV SA.

21 Rossau R, Van Heuverswijn H;

22 Rossau R, Van Heuverswijn H;

23 Rossau R, Van Heuverswijn H;

24 Rossau R, Van Heuverswijn H;

25 Rossau R, Van Heuverswijn H;

26 Rossau R, Van Heuverswijn H;

27 Rossau R, Van Heuverswijn H;

28 Rossau R, Van Heuverswijn H;

29 Rossau R, Van Heuverswijn H;

20 Rossau R, Van Heuverswijn H;

21 Rossau R, Van Benes, for detecting e.g. BORDETELLA PERTUSSIS, NEISSERIA GONORRHOEAE

25 BORDETELLA PERTUSSIS, NEISSERIA GONORRHOEAE

26 Spacer region: the 5'-end is proximal to the 16S-23S rRNA gene

27 This sequence differs in just one

28 Spacer region: the 23s rRNA gene. The sequence differs in just one

29 Position from the corresponding region in N.gonorrhoeae and this sequence which were specific for N.gonorrhoeae. A kit is provided

20 Cor detection of N.gonorrhoeae using the probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybridisation probes for detecting non-viral microorganisms -
derived from spacer region between 16S and 23S rRNA genes, for
detecting e.g. BORDETELLA PERTUSSIS, NEISSERIA GONORRHOEAE
Disclosure; Fig 3: 41pp: English.
This sequence is the non-coding strand of the 16S-23S rRNA gene
spacer region: the 5'-end is proximal to the 16S rRNA gene and the 3'-end proximal to the 23S rRNA gene. A set of probes was designed
based on this sequence which was specific for N.meningitidis. A kit
is provided for detection of this species using the probes.
Sequence 664 BP: 235 A; 123 C; 154 G; 152 T;
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.gonorrhoeae strain ITM 4367 16S to 23S rRNA gene spacer region. TRNA gene; ribosomal RNA; probe; ss. Neisseria gonorrhoeae ITM 4367. EP-452596-A.
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          DB 1; Length 603;
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                                                                                Indels
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       Score 15.6; Pred. No. 55;
                                                                            Mismatches
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                                                                                                                                                                                   206 TGCTCTACCAACTGAGCTATGC 185
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       70.9%;
81.8%;
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                                                                                                                                          1 TGTTCTACCACCTGAACTAGGC
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Q14103;
Query Match 70.9
Best Local Similarity 81.8
Matches 18; Conservative
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Best Local Similarity
Matches 18; Conserv
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base 300001 (Borrelia burgdorferi polynucleotid LOCUS X20248 Accession X20248

110000

200001 400001

100001

310000 410000 510000 610000 710000 810000 910000

500001 600001 700001 800001

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Gaps

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Indels

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Score 16.2; DI Pred. No. 52; 0; Mismatches

73.68; 85.78;

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DB 1; Length 110000;

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Sequence split into 10 fragments La Fragment Name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 63128 TGCTCTACCACCTGAGCTATG 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TGTTCTACCACCTGAACTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                   Fragment N
X20248_00
                                                                                                                                                                                                       X20248_01
X20248_02
X20248_03
                                                                                                                                                                                                                                                                                                       X20248_04
X20248_05
X20248_06
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X20248_08
X20248_09
                                                        Continuation (
WP Sequence sp
WP X20248
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                                X20248_03/c
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PT Polynucleotide(s) and proteins derived from Staphylococcus aureus - PT Polynucleotide(s) and proteins derived from Staphylococcus aureus - Stored on computer readable medium and used in the production of anti-S.aureus vaccines

PT Claim 1: Page 2593-2640: 3271pp; English.

C Taim 1: Page 2593-2640: 3271pp; English.

C This sequence represents one of 5191 Staphylococcus aureus DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access to medium, preferably selected from a floppy or hard disk, random access the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are including entities and these polypeptides can composition against S.aureus infection. The be used in a vaccine composition against S.aureus infection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, concluding cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can also mean a reinare or number of number for isolating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inote "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus config SEQ ID #3678.
Computer readable medium; vaccine; S.aureus infection; immunodetection;
cellulitis: eyelid infection; food poisoning; osteomyelitis; therapy;
skin infection; surgical wound infection; scalded skin syndrome;
toxic shock syndrome; ds.
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for isolating
                                                                                                                                                                                         ö
                     698 T;
                                                                                                                     DB 1; Length 4190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (and their fragments) are useful as primers or probes for isc
homologues of any of the S aureus DNA sequences contained on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.6%; Score 16.2; DB 1; Length 648; 81.8%; Pred. No. 28; tive 0; Mismatches 4; Indels
                                                                                                                                                                                     3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 G;
                                                                                                          Score 16.2; DE
Pred. No. 35;
0; Mismatches
          1406 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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0
                                                                                                                                                                                                                                                                                     3522 GTTCTACCTCCTGCACCAGGC 3502
                                                                                                                                                                                                                                2 GTTCTACCACCTGAACTAGGC 22
       780 A;
                                                                                                          73.68;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V77989 standard; DNA; 648 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121. .180
/*tag= a
                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
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   4190 BP;
                                                                                            Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JAN-1997; 100117
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Best Local Similarit,
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-1996;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA;
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V77989
V77989
V77989
V77989
V77980
V77980
V77980
V77980
V77980
V77990
V77900
V7
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Class I 1991-tRNA synthetase useful for treating infections by Borrella or Treponema

Example 3: page 49: 51pp: English.

Example 3: page 49: 51pp: English.

The present invention describes class I-type lysyl-tRNA synthetase (I).

(I) is used: (i) to diagnose infection by pathogens that express (I) but of class II-type lysyl-tRNA synthetase (Ia), particularly infections by Borrella or Treponema, specifically Lyme disease or syphilis; and (ii) to screen for specific inhibitors of (I), potentially useful as therapeutic agents in human and veterinary medicine. Nucleic acid encoding (I) is used as a source of probes for diagnosing infection by (I) producing pathogens. Since (I) is fundamentally different from the class II enzyme (Ia) producing hosts or beneficial microorganisms. The present sequence represents Borrella burgdorferi t-RNA synthetase Lysl DNA sequence, from an example of the present invention.

Sequence 73 BP: 13 A; 17 C; 23 G; 20 T;
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                                                    23-JUN-1999 (first entry)

Borrella burgdorferi t-RNA synthetase Lysl DNA sequence.

Class I-type Lysyl t-RNA synthetase; Lyme disease; syphilis; infection;

Methanococcus maripaludis; Borrelia burgdorferi; Treponema;

antibacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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85.7%; Pred. No. 21;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               026727/c
ID 026727 standard; DNA; 7753 BP.
AC 026727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
X30293 standard; DNA; 73 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGTTCTACCACCTGAACTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAR-1999.
09-SEP-1998; U18968.
10-SEP-1997; US-058420.
(UYXA ) UNIV YALE.
1bba M, Soell D;
WPI; 99-215059/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                          Borrella burgdorferi.
WO9913057-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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Gaps

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1 TGTTCTACCACCTGAACTAGGC 22

Conservative

10 TGNTCTACCAATTGAGCTAGGC

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RESULT

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P-PSDB; W59358
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                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     V34854;
                                                                                                                                                                                                                                                                                                                                                                          RESULT
V34854/c
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                                                                                                                                                                                                                                            claim 1; Page 898-902; 2084pp; English.

Claim 1; Page 898-902; 2084pp; English.

A computer readable medium has been developed which has recorded on it 92 nucleotide sequences isolated from the Enterococcus facealis genome.

X12938 to X13919 represent these nucleotide sequences which are primary can identify fragments of the Enterococcus facealis genome with commercial importance. The products can be used to detect the presence of Enterococcus facealis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus facealis, or another related organism, in vivo or in vitro. In particular the control of prevent or another or another or another or another coccus facealis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1924; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer readable medium; vourly only 11330.
Computer readable medium; voulle; S. autrous infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
Staphylococcus aureus.
EP-786519-A2.
                                                                                                                                                                                          WPI: 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides used to develop products for the detection of Enterococc s and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
          19-WAR-1999 (first entry)
Enterococcus faecalis genome contig SEQ ID NO:159.
Enterococcus faecalis; contig; detection; Enterococcal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.8; DB 1; Length 8160;
Pred. No. 19;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1654 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1463 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus contig SEQ ID #1336.
                                                                                          12 NOV-1998.

04-MAY 1998; U08985.

14-NOV-1997; US-066009.

06-MAY 1997; US-044031.

16-MAY 1997; US-044655.

(HUMA-) HUMAN GENOME SCI INC.

BATASh, SC., DILLON PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2731 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3366 TGITCTAGCICCTGAACTAG 3385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V75647 standard; DNA; 633 BP. V75647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGTTCTACCACCTGAACTAG 20
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O7-JAN-1997; 100117.
O5-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 90.09
Matches 18; Conservative
                                                               Enterococcus faecalis. W09850555-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8160 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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V75647C
ID V756.
AC V756.
AC V756.
BDT 16-M.
KW Complex
KW Complex
KW Complex
KW Complex
COC This
COC Medi
g
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New nucleic acid encoding human retinal degradation polypeptide -
The present seed to diagnose neurological disease and to identify
and related probes, vectors, transformed cells, proteins and
antibodies, used to diagnose neurological disease and to identify
specific modulators with possible therapeutic activity
by specific modulators with possible therapeutic activity

Disclosure; page 36-37; 59pp; Englash.

CC The present sequence represents the human retinal degeneration B2 cDNA
(hrdgB2), the product of which is a non-receptor tyrosine kinase binding
CC protein. The isolation of this cDNA involved the amplification of an EST
CC subcloned, sequenced and then used as a probe to secreen a human fetal
C brain cDNA library. The clone obtained was used as a probe to rescreen
the same library, from this seven clones were found, subcloned and
C brain cDNA library. The clone obtained was used as a probe to rescreen
the same library from this seven clones were found, subcloned and
C brain cDNA library. The clone obtained was used as a probe to rescreen
the same library from this seven clones were found, subcloned and
C protein has been found to be expressed in the brain, heart, thymus and
C peripheral blood leukocytes, it contains a PIT domain, and a Pyk2 binding
CC domain and is thus concerned with recycling synaptic vesicles and
regulating neurotransmitter signalling respectively. This protein is
C seen to be involved in signalling reasectively. This protein
C would be useful in diagnosis, treatment, and prevention of the following
C diseases: myasthenia qravis; neuroblastoms; thrombosytopaenia; stroke;
                            That protein encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a Rit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences fond their fragments) are useful as primers or probes for isolating computer redable medium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human retinal degeneration B2 polynucleotide (hrdgB2).

Non-receptor tyrosine kinase binding protein; screening; brain; heart; thymus; leukocytes; human fetal brain; PIT domain; Pyk2 binding domain; synaptic vesicles; neurotransmitter signalling; myasthenia gravis;
S.aureus DNA sequences allows putative functions to be assigned so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stroke; neuroblastoma; thrombocytopaenia; Alzheimer's; Huntington's;
Parkinson's; depression; schizophrenia; pain epilepsy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alzheimer's; Huntington's; Parkinson's; depression; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.5%; Score 16.4; DB 1; Length 633; 94.4%; Pred. No. 22; ive 0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "hrdgB2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
174. .3908
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WPI; 98-251286/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V34854 standard; cDNA; 4190 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 TGTGCTACCACCTGAACT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TGTTCTACCACCTGAACT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1998 (first entry)
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-027337.
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11-OCT-1996; US-027
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Page 15: 99-153692/13.

New isolated nucleic acid encoding the new human cytokine Tango-77 - New isolated nucleic acid encoding the new human cytokine Tango-77 - BT New isolated nucleic acid encoding the new human cytokine Tango-77 - Stample 5; Figure 3: 226pp; English.

X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences containing alternatively spliced forms of human IL-Ira. Such fragments are used in the method of the invention which describes the isolation of a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a confiammation by binding to the interleukin-1 receptor (IL-IR). It may also bind to a new receptor so could regulate other cellular processes conditional interleukins, especially in the new conditions also bind to a new receptor so could regulate other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and inflammatory bowel disease. It may also induce or suppress interleukins, cytokines and conditions associated with abnormal levels of inflammation, or activity
                                                                                                          Sumption occurs. Since the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human IL-1ra BAC contiguous DNA sequence 33.

Hango-7; human; IL-1ra: cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; requlation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; Homo sapiens.

Homo sapiens.

W09906426-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Predicting increased risk of sight-threatening diabetic retinopathy - comprises identifying genetic polymorphism pattern for genes IL-IA, IL-IB and IL-IRN, useful to allow treatment before clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 22; DB 1; Length 27; 100.0%; Pred. No. 0.025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-FEB-1999.
03-AUG-1998; U16102.
02-3UL-1998; U5-01560.
04-AUG-1997; US-054646.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC. Pan Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL-1 or its receptor complex. quence 5701 BP; 1729 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-1999 (first entry)
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Best Local Similarity
Local 22; Conserve
                                                                                          symptoms occur
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When we though of determining a patient's susceptibility to inflammatory disorders - by detecting the presence of an IL-1 (44112332)

The property is detecting the presence of an IL-1 (44112332)

The property is designing treatment strategies that modulate

The activity of proteins produced by the IL-1 gene cluster

CC A method has been developed for determining a patient's susceptibility

CC A method has been developed for determining a patient's susceptibility

CC A method has been developed for determining a patient's susceptibility

CC A method has been developed for determining a patient's susceptibility

CC A method has been developed for determining a patient's susceptibility to an inflammatory

CC patient, where its presence indicates susceptibility to an inflammatory

CC disorder. X16607 to X16631 represent PCR primer used in the method for

CC detecting the IL-1 (44112332) haplotype. The method provides kits for

CC detecting the IL-1 (44112332) haplotype. The method provides kits for

CC disorders, including coronary artery disease, osteoporosis, nephropathy

CC disorders, including coronary artery disease, osteoporosis, nephropathy

CC disorders, including coronary areata, Graves disease, systemic lupus

CC alabettes mellitus, alopecia areata, Graves disease, systemic lupus

CC disorders, including diabetic retinopathy, juvenile chronic arthitis,

CC allowed insulin dependent diabetes. The identification of a

CC ausative, and this information is useful in designing treatment

CC causative, and this information is useful in designing treatment

CC some alleles from the IL-1 gene cluster are associated with particular

CC fone alleles from the IL-1 gene cluster are associated with particular

CC fone alleles is useful in determining genetic susceptibility to

CC inflammatory diseases, including those with a moliven component component.
                                                                                                                                                                                                                                                                29-APR-1999 (first entry)
Interleukin 1 (44112332) haplotype PCR primer #5.
Interleukin 1: IL-1; haplotype; inflammatory disorder; alopecia areata; coronary artery disease; osteoporosis; nephropathy; diabetes mellitus; Graves disease; systemic lupus erythamatosus; lichen sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                             Gaps
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                   Pred. No. 0.049; Mismatches 0; Indels
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7. Pred. No. 0.075;
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G;
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29-MAY-1997; GB-011040.
(CAMY) CAMP N J.
(GOXA/) COX A.
(DGIO/) DE GIOVINE F S.
(DUFF/) DUFF G.
Camp NJ, COX A, De Giovine FS, Duff G;
                                                                                                                                                                                                                                                                                                                                                                       ulcerative colitis; PCR primer; ss Synthetic.
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C;
100.08; Pr.
                                                                                                    431 IGTTCTACCACCTGAACTAGGC 452
                                                                            1 TGTTCTACCACCTGAACTAGGC 22
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                 Best Local Similarity 100.
Matches 22; Conservative
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Best Local Similarity 100.
Matches 21; Conservative
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Sequence 21 BP;
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WO9854359-A1.
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DB 1; Length 5701; 100.0%; Score 22;

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**Ouery Match** 

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic . nucleic search, using sw model

September 18, 1999, 05:27:23; Search time 213.04 Seconds (without alignments) 25.837 Million cell updates/sec Run on:

Title: US-09-037-472-7
Perfect score: 22
Sequence: 1 TGTTCTACCACCTGAACTAGGC 22

Scoring table: IDENTITY\_NUC

311585 seqs, 125096042 residues Searched:

N\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES		r for de	nterleukin-	IL-1ra	eukin 1	nterococcus fa	ylococcus	uman retinal d	sn:	Continuation (4 of Rorrelia hundorfo	odes exons XV	orrhoeae str	meningitidis	.gonorrhoeae	treptococcus	treptococcus p	Staphylococcus aur	Staphylococus aur	Staphylococcus aur	Stanhylococus aur	Staphylococcus aur	Stabbylococcus aur	taphylococcus	taphylococcus	taphylococcus	aphylococcus	phylococcus	nterococcus f	nterococcus fae	Enterococcus faeca								
SUMMARIES	ID	T70316		X02988			5) (	V34854	٠.	0293		014102				V52232		$-\infty$	œ	œ	യ	V/8001	~ r	. ^		V77853	~ <	V/88// V79855	o 0	മെ	œ	œ	œ	œ	∞ ₁	3	X13384	ກເ
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Encodes Xenopus Bo Sequence encoding	to periodontal disease. is; polymorphism; ta; IL-1B; primer; PCR; severity ed in a new method periodontal disease by in the gene sequences tin-1 beta (IL-1B); identified as IL-1B; in the polymorphism inc (C/T) polymorphism	i; Length 22; 0; Indels 0; Gaps 0; c; amplification; cleukin-l-alpha;
44 15.2 69.1 1992 1 Q10895 45 15.2 69.1 3565 1 Q84051 ALIGNMENTS	PESULT 1  T70316 standard; DNA; 22 BP.  AC 770316; DT 10-OCT-1997 (first entry) DE Primer for detecting genetic predisp_sition to periodontal disease.  KW Prindental disease; gingivitis; pariocontitis; polymorphism; KW prindental disease; gingivitis; pariocontitis; polymorphism; KW polymerase chain reaction; ss.  Synthetic.  PN W99705180-Al.  PP C 7-4UG-1995; US-510696.  PA (KDZI)-YOKORNAM K S.  CC of interleukin-1 alpha (IL-IA)-and interleukin-1 beta (IL-IB)-CC of interleukin-1 alpha (IL-IA)-ADA (IL-IB)-CC of interleukin-1 alpha (IL-IA)-CC of interleukin-1 alpha (IL-IA)-CC of	Query Match Best Local Similarity 100.0%; Score 22; DB 1; Length 22; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 22; Conservative 0; Mismatches 0; Indels 0;  Qy 1 TGTTCTACCACCTGAACTAGGC 22

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| 9ene | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..8073 | 7825..807
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Direct Submission
Submitted (10-NOV-1995) K.V. Kowallik, Heinrich-Heine Universitaet
Duesseldorf, Universitaetsstr. 1 Geb.26 13/02/46, D- 40225,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast Odontella sinensis
Eukaryota: stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
1 (bases 1 to 119704)
Kowallik,K.V., Stoebe,B., Schaffran,I., Kroth-Pancic,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Chloroplast Genome of a chlorophyll a+c- containing Alga
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Plant Mol. Biol. Rep. 13, 336-342 (1995)
2 (bases 1 to 119704)
Kowallik,K.V.
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SOURCE

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165 ribosomal RNA: 165 rRNA gene; 235 ribosomal RNA; 235 rRNA gene; 305 ribosomal RNA: 165 rRNA gene; 305 ribosomal protein S11; 305 ribosomal protein S12; 305 ribosomal protein S12; 305 ribosomal protein S14; 305 ribosomal protein S14; 305 ribosomal protein S16; 305 ribosomal protein S17; 305 ribosomal protein S17; 305 ribosomal protein S19; 305 ribosomal protein S2; 305 ribosomal protein S2; 305 ribosomal protein S3; 305 ribosomal protein S3; 305 ribosomal protein S6; 305 ribosomal protein S1; 305 ribosomal protein S1; 305 ribosomal protein L12; 505 ribosomal protein L13; 505 ribosomal protein L13; 505 ribosomal protein L13; 505 ribosomal protein L11; 505 ribosomal protein L12; 505 ribosomal protein L13; 505 ribosomal protein L13; 505 ribosomal protein L13; 505 ribosomal protein L15; 505 ribosomal protein L15; 505 ribosomal protein L15; 505 ribosomal protein L20; 505 ribosomal protein L21; 505 rib
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          FRG
f.Molekulare Genetik, Ihnestrasse 73, D-1000 Berlin 33,
Location/Qualifiers
1..1895
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Pred. No. 1.8e+02;
); Mismatches 2; Indels
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1268. .1885
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/gene="RPL19"
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90.0%;
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/gene="nusG"
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267753.1 GI:1185127
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Matches 18; Conserv
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complement(5945. 6313)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Synechocystis sp. genes rpl19, transfer RNA-Trp and nusG
X72627
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Submitted (16-MAR-1993) J. Schmidt, Max-Planck-Institut
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Schmidt, J. and Subramanian, A.R.
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Pred. No. 1.3e+02;
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93281410
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Schmidt,J.
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/
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PSHADATYEAKYGIRNWQGGGRSSARETIGRVAAGAIAKKILAOFNGVEIVAYVKSIO
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EELOKGMADFDVLJATDPMARE TARLGKOLGPRGLMPSPRGGTVTADLAAAVNEERAG
KLEFRADRTGIVHVMFGKASFSADDLLANLKALOETIDRNRPSGAKGRFWRTYVSSS
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TRANKFGMIIPVEISYFEDRSFIFILKTPPAGYLIRRAAGVEKGSSEPNKNKVASITR
EQLREIAOTKLPDLNANDIDAAMNIIEGTARNMGITVNS"
COMPLEMENT (4 SOI. . 5118)
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/transl_table=11
/product="50S ribosomal protein L1"
/protein_id="BAA17418.1"
/db_xref="PID:d1018151"
/db_xref="PID:d1018151"
/db_xref="FID:d1018151"
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/product="50S ribosomal protein L12"
/protein_id="BAA17416.1"
/db_xref="PID:d1018149"
/db_xref="PID:q1652495"
/db_xref="GI:1652495"
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/product="50s ribosomal
/protein_id="BAA17419.1"
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complement(1929. .2315)
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complement(2403. .2924)
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/gene="rpl1"
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/gene="rpl11"
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                                                                                                                                                                                                                                                                                                   Camingase; excludicases ABC subunit A; ferredoxin; glucose of phosphate dehydrogenase; glutaredoxin 3; glutathione synthetase; glycoprotein 64; high light inducible protein; histidinol-phosphate alminotransferase; hydrogenase expression/formation protein HypE; hitate transfert 45kD protein; nitrate transport protein NrtB; nitrate transport protein NrtB; peptide-chain-release factor 3; phosphoribosyl aminoidazole succinocarboxamide synthetase; poly(3-hydroxyalkanoate) synthese; polypeptide deformylase; protein kinase C inhibitor; protein kinase polypeptide deformylase; protein kinase C inhibitor; protein kinase nucleotide transhydrogenase alpha subunit; pyruate dehydrogenase El beta subunit; rare lipoprotein A; regulatory components of protein SoED; succinate dehydrogenase flavoprotein system; secreted protein MBPO; secretory protein SoED; succinate dehydrogenase flavoprotein subunit; transfordet in transfordet in transfordet in transfordet in spice flavoprotein E. Synechocystis sp. (strain:PCC6803) DNA.

Synechocystis sp.
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
carbon dioxide concentrating mechanism protein Ccmk; carboxyl-terminal protease; cell division FtsZ protein; cell division protein FtsB; ofloroplast division protein FtsB; ofloroplast import-associated channel IAP75; chorismate synthase; cysteine synthase; cytoplasmic membrane protein for maltose uptake; oytosine deaminase; exclinclease ABC subunit A; ferredoxin; glucose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (28-JUN-1996) to the DDBJ/EMBL/GenBank databases. Satoshi
Tabata, Kazusa DNA Research Institite, Laboratory of Gene Structure
22: 1523-3, Yanauchino, Kisarazu, Chiba 292, Japan
(E-mail:tabata@kazusa.or.jp, Tel:+81-438-52-3933,
Fax:+81-438-52-3934)
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/db_xref="PlD:d1018147"
/db_xref="PlD:g1652493"
/db_xref="C1:162493"
/translation="MGETKLTADQRWQGTHDCKDYILSYIELHRRYELEVEVVASFWP
HVPPEKKTLLAWEKELILKARSPFNKECWRWWGQPFGKLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential protein coding regions were assigned on the basis of similarity search of the ORFs and GeneMark analysis.
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/db_xref="PID:d1018148"
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/note="ORF_ID:ss13712"
/codon_start=1
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/codon_start=1
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/db_xref="taxon:1143"
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MEDLINE JOURNAL

COMMENT

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Query Match
Best Local Similarity
Matches 19; Conserv
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D90906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For more information about this sequence or the Leishmania Project, see http://www.sanger.ac.uk/Projects/L_major.

order of segments is not known: 800 n's separate segments.

* NOTE: This is a "working draft" sequence.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leishmania major chromosome 4 clone L1156 strain Freidlin, WORKING AL034390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Mar 21, 1999 this sequence version replaced gi:4225966. IMPORTANT: This sequence is unfinished and does not necessarily
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                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murphy,L., Quail,M., Lawson,D., Harris,D., Rajandream,M.A.,
Ivens,A. and Barrell,B.G.
Direct Submission
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                                                                                                                                                                                                                                                                      Length 300;
                                                                                                                                                                                                                                                                                                         Indels
1. .300
/organism="Mycoplasma capricolum"
/strain="Kid; ATCC 27343"
/db_xref="taxon:2095"
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                                                                                                                                                                                                                                                                      Score 17.2; DB 1;
Pred. No. 1.3e+02;
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                                                                                                                                            /note="Trp-tRNA(TCA)"
166. 240
/note="Trp-tRNA(CCA)"
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10916 c 11922 g
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                                                                                                                                                                                                                                                                                                                                                          1 TGTTCTACCACCTGAACTAGGC 22
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HTG: HTGS_PHASE1.
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Best Local Similarity 86.4
Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserv
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91652492
D90906.1 G1:1652492
D90906.1 G1:1652492
D-hydroxy-6-oxohepta-2,4-dienoate hydrolase; 50S ribosomal protein L1: 50S ribosomal protein L10; 50S ribosomal protein L11; 50S ribosomal protein L12; 50S ribosomal protein L19; AEC transporter; ATP-dependent DNA helicase RecQ; CbiD protein; DNA binding protein H0; DNA helicase II; DNA-damage-inducible protein; LPS glycosyltransferase ICsA; NADH dehydrogenase subunit L8; NADH dehydrogenase subunit L8; NADH apoprotein subunit L11; DNA polymerase sigma-E factor; RfbJ protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understranding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For more information about this sequence or the Leishmania Project, see http://www.sanger.ac.uk/Projects/L_major.
order of segments is not known; 800 n's separate segments.
* NOTE: This is a 'working diaft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                 Leishmania major chromosome 4 clone L684 strain Freidlin, WORKING AL034360
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On Mar 24, 1999 this sequence version replaced gi:4469263.
IMPORTANT: This sequence is unfinished and does not necessarily
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Synechocystis sp. PCC6803 complete genome, 8/27, 920916-1056466.
D90906 AB001339
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Ivens, A. and Barrell, B.G.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 87;
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DD 39250 TGTTCTACCACATAAACAAGGC 39271
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illarity 86.4%;
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HTG; HTGS_PHASE1.
Leishmania major.
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ö g150214 K02974.1 GI:150214 transfer RNA: transfer RNA-Trp. '--lum (American type culture collection 27343) DNA, clone Gaps 12-AUG-1994 Mycoplasma capricolum Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; ; Score 17.2; DB 1; Length 76; Pred. No. 1.4e+02; 0; Mismatches 3; Indels BCT MYCTGW 994 bp DNA Mycoplasma capricolum Trp-tRNA genes. K02974 capricolum group. 9150214 K02974.1 DEFINITION ORGANISM ACCESSION KEYWORDS SOURCE NID VERSION

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Location/Qualifiers

FEATURES

Even though 'tga' is a nonsense or termination (opal) codon throughout prokaryotes and eukaryotes, it codes for tryptophan in M.capricolum, as is the case in mitochondria. The sequence of the S3 and L16 ribosomal protein genes from this wall-less bacterium include 'tga' codons in their reading frames in positions corresponding to tryptophan in E.coli S3 and L16 genes. A Trp-tRNA with the opal suppressing anticodon 'tca' is found in M.capricolum dyad symmetry, which could be a transcription-termination structure is found at positions 614-640. .. 0 1 (bases 1 to 994)
Yamao,F., Muto,A., Kawauchi,Y., Iwami,M., Iwagami,S., Azumi,Y. and Yamao, F., Muto, A., Kawauchi, Y., Iwami, M., Iwagami, S., Azumi, Y. and (bases 1 to 300) Muto, A., Andachi, Y., Yuzawa, H., Yamao, F. and Osawa, S. The organization and evolution of transfer RNA genes in Mycoplasma MYCTRGC2T 300 bp DNA BCT 02-FEB-1999 Mycoplasma capricolum tRNA gene cluster encoding two Trp-tRNAs. D00551 These data kindly submitted in computer readable form by: Akira Gaps Mycoplasma capricolum Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Draft entry and reprint for [1] kindly provided by F.Yamao, 20-SEP-1985. Department of Biology, School of Science, Nagoya University Furo-cho, Chikusa-ku ·: UGA is read as tryptophan in Mycoplasma capricolum Proc. Natl. Acad. Sci. U.S.A. 82 (8), 2306-2309 (1985) Length 994; UGA is read as tryptophan in Mycoplasma capricolum Proc. Natl. Acad. Sci. U.S.A. 82, 2306-2309 (1985) Mycoplasma capricolum (strain:Kid; ATCC 27343) DNA. Indels 416. .491 /note="codon recognized: TGA; Trp-tRNA" Nucleic Acids Res. 18 (17), 5037-5043 (1990) 1. .994 /organism="Mycoplasma capricolum" /db\_xref="taxon:2095" 78.2%; Score 17.2; DB 1; 86.4%; Pred. No. 1.2e+02; Live 0; Mismatches 3; ىد 379 345 a 125 c 145 g 153 bp upstream of AluI site. /product="tRNA-Trp" 529. 602 052-781-5111 x6642 052-783-0719. /note="Trp-tRNA" 125 c 145 441 IGITCIACCIACIGAACIAIGC 420 22 1 TGTTCTACCACCTGAACTAGGC g216805 D00551.1 GI:216805 capricolum group. 1 (bases 1 to 300) Query Match
Best Local Similarity 86.4 Matches 19; Conservative Nagoya 464-01 capricolum Proc. Nat 85190486 tRNA-Trp. Osawa, S. Osawa, S. 85190486 90384798 Japan Phone: MYCTRGC2T/c BASE COUNT ORIGIN DEFINITION JOURNAL RESULT 10 ORGANISM REFERENCE AUTHORS **trna** TITLE JOURNAL MEDLINE REFERENCE AUTHORS JOURNAL MEDLINE COMMENT **trna** ACCESSION REFERENCE AUTHORS FEATURES TITLE KEYWORDS COMMENT TITLE VERSION q

us-09-037-472-7.rge

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247. .273
/note="pot.stem-loop structure; terminator-like structure"
261. .273
                                                                                                                                                                                                                                           Evolutionary dynamics of tryptophan tRNAs in Mycoplasma capricolum Mol. Gen. Genet. 212 (2), 364-369 (1988)
88302126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="pot.stem-loop structure; terminator-like structure"
                                                   MUCOPLASMA CAPTICOLUM GENES for tRNA-Trp (UCA) and tRNA-Trp (CCA). X07691
                                                                                                                                                                                            capricolum group.
1 (bases 1 to 281)
Yamao,F., Iwagami,S., Azumi,Y., Muto,A., Osawa,S., Fujita,N. and
                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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/note="transfer RNA-Trp (CCA)"
194. 196
/note="transfer RNA-Trp (CCA) anticodon"
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Data kindly reviewed (27-JUL-1988) by YAMAO F.
Location/Qualifiers
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Mycoplasma capricolum transfer RNA-Trp (UCA).
g44265
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/db_xref="taxon:2095"
/clone="pMCH964"
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/note="transfer RNA-Trp (UCA)"
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/note="inverted repeat B'"
50 c 57 g 94 t
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/note="inverted repeat A"
147. 155
/note="inverted repeat A'"
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27.32
//note"put. 10 region"
39.278
//note"transcript"
                                                                                                                                transfer RNA; transfer RNA-Trp.
Mycoplasma capricolum.
Mycoplasma capricolum
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X07691.1 GI:44254
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Best Local Similarity
Matches 19; Conserv
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MCTRNW12/c
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Location/Qualifiers
1. .76
                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia.

1 (bases 1 to 76)
Eisenberg, S.P., Yarus, M. and Soll, L.
The effect of an Escherichia coli regulatory mutation on transfer RNA structure
                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
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Pred. No. 1.4e+02;
0; Mismatches 3; Indels
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/product="tRNA-Phe"
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/db_xref="taxon:562"
1. .76
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E.Coli Trp-tRNA suppressor mutant.
M25066
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80117855
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M25066.1 GI:174466
transfer RNA-Trp suppressor.
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/mod_base=OTHER
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54
                                                             /mod_base=p
15 a 21 c
5' end of mature tRNA.
                         /mod_base=t
55
                                                                                                                                       Query Match 78.2%;
Best Local Similarity 86.4%;
Matches 19; Conservative
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Best Local Similarity 86.4%;
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complement(52991. 53050)

/note="MIR repeat: matches 234. .175 of consensus"
/note="MEA3" .60997)

/note="MEA3" .60997)

/note="MEA3" repeat: matches 524. .480 of consensus"
/note="MEA3" repeat: matches 409. .251 of consensus"
/note="MIR2" repeat: matches 32. .142 of consensus"
/note="MIR2" repeat: matches 32. .142 of consensus"
/note="MIR3" repeat: matches 301. .6 of consensus"
/note="MEA3" repeat: matches 48. .409 of consensus"
/note="MER3" repeat: matches 48. .409 of consensus"
/note="MER3" repeat: matches 48. .525 of consensus"
/note="MER3" repeat: matches 4. .1372 of consensus"
/note="match: STS 65881)
/note="match: STS 65881)
/note="match: STS 65830;
/note="match: STS 668450;
/note="match: STS 668450;
/note="matches 300. .1 of consensus"
/note="matches 3768. .3579 of consensus"
/note="laludp repeat: matches 3768. .3579 of consensus"
/note="matches 3768. .3579 of consensus"
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16S ribosomal RNA: 23S ribosomal RNA; SS ribosomal RNA; ribosomal RNA: transfer RNA: transfer RNA-val.
euglenophycean alga.
Chloroplast Astasia longa
Eukaryota; Euglenozoa; Euglenida; Euglenales; Astasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Siemeister, G.
Submission
Submission
Submission
Submisted (08-FEB-1989) Siemeister G., Botanisches Institut der Universiteit, Kirschallee 1, D 5300 Bonn 1, FKG
C. (bases 1 to 6081)
Siemeister, G. and Hachtel, W.
Organization and nucleotide sequence of ribosomal RNA genes on a circular 73 kbp DNA from the colourless flagellate Astasia longa 90291517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Astasia longa chloroplast ribosomal DNA.
X14386
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95.0%; Pred. No. 20;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="23S ribosomal RNA"
3252. .3382
/note="5 ribosomal RNA"
3674. .3746
/note="tRNA-Val"
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/db_xref="taxon:3037"
34. .3137
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1. .6081
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Contributed on tape April 1983 by M.Sprinzl & D.H.Gauss; from their entries 1810, 1811, 1814 in Nucleic Acids Res. 11, r1-r54 (1983). [1] suggests that 'uga' suppression is carried out by a Trp-tRNA whose anticodon-recognition is altered by a change outside the anticodon. [2] discusses the mutational effects on the in vitro and in vivo properties of Trp-tRNA.
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Eisenberg, S.P., Soell, L. and Yarus, M.
The purification and sequence of a temperature-sensitive tryptophan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9174464
K00260.1 GI:174464
transfer RNA; transfer RNA supressor; transfer RNA-Trp.
Escherichia coli ([1]: wild-type strain CA244, uga-suppressor
strain caj64; [2]: wild-type strain LS 340, temperature-sensitive
strain LS 874) tRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="codon recognized: TGG; Trp-tRNA (NAR: 1810)"
/product="tRNA-Trp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="g in wild-type; a in ts mutant ls 874 [2]"
                                                                                                                                                                                                                                  ó
                                                                                                                                                                                       Length 6081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 E.coli Trp-tRNA; also ts and uga-suppressor mutations.
K00260
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/organism="Escherichia coli"
//db_xref="taxon:562"
1..76
                                                                                                                                                                           79.1%; Score 17.4; E
94.7%; Pred. No. 81;
Live 0; Mismatches
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79194094
3860. .5379
/note="16S ribosomal RNA"
5535. .>6081
/note="23S ribosomal RNA"
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J. Mol. Biol. 58, 439-458 (1971)
                                                                                       1301 g
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Hirsh, D.
                                                                                                                                                                                                                           18; Conservative
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.303 of consensus"

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/note="MER218 repeat: matches 792. .4 of consensus" 17480. .17647
/note="AluSp repeat: matches 136. .303 of consensus" complement(19382. .19433)
/note="List repeat: matches 578. .526 of consensus" complement(1956. .19960)
/note="List repeat: matches 300. .1 of consensus" complement(2956. .19960)
/note="Alus repeat: matches 300. .1 of consensus" complement(2914. .23103)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3005...3913)

complement(33402...33698)

complement(33402...33698)

complement(33402...33698)

complement(3447...38699)

complement(4347...38699)

complement(40249...40548)

complement(40349...40548)

complement(41636...41692)

complement(41636...4166)

complement(40393...4166)

complement(41636...4166)

complement(41636...4166)

complement(41636...4166)

complement(41636...4166)

complement(416374...48264)
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/note="WRR42c repeat: matches 348. .1536 of consensus"
50415. .50724
                                                                                                                                                             50415. .50724
/note="AluJo repeat: matches 2. .302 of consensus"
complement(50998. .51085)
/note="MIR2 repeat: matches 145. .58 of consensus"
complement(52655. .52797)
/note="LIME2 repeat: matches 699. .554 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24161. .24346
/note="L1 repeat: matches 4042. .4231 of consensus"
4420. .24689
/note="AluJo repeat: matches 1. .302 of consensus"
24771. .25083
/note="AluSq repeat: matches 2. .303 of consensus"
             complement(12599. .12717)
/note="MIR2 repeat: matches 146. .28 of consensus"
15448. .15519
/note="MIR2 repeat: matches 74. .146 of consensus"
complement(15866. .16333)
/gene="dJ501N12.1"
          12599. .12717)
.repeat: matches 146. .28 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26805. .26904

/note="MIR repeat: matches 35. .134 of consensus" complement(27877. .28054)
/note="MIR repeat: matches 260. .77 of consensus" 28097. .28238
/note="MIR repeat: matches 71. .201 of consensus" complement(28312. .28688)
/gene="dJ50]N12.1.
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/gene="dJ501N12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: GSS AQ020591"
complement(30856. .30913)
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complement(48410, .49073)
/gene="dJ501N12.2"
49166, .50348
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                  repeat_region
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only a small overlap as described above. This sequence is the entire insert of clone 501M12. This sequence has been finished according to sequence and criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed in collaboration by the Sanger Centre chromosome 6 mapping group and Armin Volz 6 Andreas Ziegler. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6/501M12 is from the library RPCI3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
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AIQEDLKSABRIAMRDAKNSKTLLPNLYHYGGASWAGASGLLSSPIQFTLESMAGEVTR
VVDGQLKALLESMYDAABULCPNVMKAHIRQDLIHASTEKISIPRTFVKNYLLEQSG
IDILMKISEVKLTYASFLSDRIVDEILDALSHCHHKLADHFSRRGKTLPQQESLEIEL
AEEKPVRRSIITVEELTEIERLEDLDTCM"
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7659. 7776
/note="AluYb8 repeat: matches 191. .308 of consensus"
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joint(<6829 . 6895,15857. 15985,17949. 18080,28912.
32011. 32098,34703. >34852)
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//note="Aluab repeat: matches 280. .1 of consensus"
complement(1341. .1477)
//note="MIR_repeat: matches 237. .85 of consensus"
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/note="AluSg repeat: matches 1. .239 of consensus"
complement(8536. .8952)
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complement(9800. .10072)
/note="AluSx repeat: matches 273. .1 of consensus"
complement(10099. .10222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4030. .4359
Anote-"Aluy repeat: matches 1. .296 of consensus"
complement(4554. .4853)
Anote-"Aluyo repeat: matches 301. .1 of consensus"
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/chromosome="6"
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/clone_lib="RPCI3"
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/gene="dJ501N12.1"
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HSIL1AG

RESULT

QQ à

TITLE

SOURCE

COMMENT

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Submitted (06-JUL-1998) E-mail enquires: humquery@sanger.ac.uk clone requests: clonerequest&sanger.ac.uk clone requests: clonerequest&sanger.ac.uk clone requests: clonerequest&sanger.ac.uk clonered.ii 1998 this sequence version replaced gi:2980811. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene. Contains ESTs, STSS and GSSs, complete sequence.
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                          4893. .5174
/note="Alu repetitive sequence"
6262. .6432
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11863. 11970
/note="Alu repetitive sequence"
1 2489 c 2226 g 3547 t
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/note="poly[dA-dC] tract"
8912. .9137
/note="5 x 46 bp repeat"
9770. .9806
/note="poly [dT-dG] tract"
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/note="poly [dA-dC] tract"
7815..7939
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                                              .4102
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Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 11970)
Furtuni,Y., Notake,M., Fukui,T., Ohue,M., Nomura,H., Yamada,M. and
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DSEEEIIKPRSSPFSFLSNVKYNFMRIIKYEFILNDALNGSIIRANDYLLTAALHNL
DEAVKFDMGAYKSSKDDAKIIVILRISKTQLYVTAQDEDQPVLLKEMPEIPKTITGSE
TNLLFFWETHGTKNYFTSVAHPNLFIATKQDYWVCLAGGPPSIIDFOILENQA"
         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erratum:[[published erratum appears in Nucleic Acids Res 1986 Jun
25:14(12):5124]]
Data kindly reviewed (10-NOV-1986) by Y. Furutani.
                                                                                                                                                                                                                                                                                                                                                                                                                                Complete nucleotide sequence of the gene for human interleukin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /254...393
/note="Alu repetitive sequence"
1375...1382
/note="pot transcription activator (seq. homolog. to
adenovirus 2 major late promoter transcription factor
                                                                                                                                                                                                                                                           Alu repetitive sequence; interleukin l alpha; inverted repeat; repetitive sequence.
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       Gaps
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/codon_start=1
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       ö
       Indels
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Human gene for interleukin 1 alpha (IL-1 alpha).
X03833
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/note="inverted repeat A"
1383. .1390
/note="inverted repeat A'"
1383. .1390
/note="direct repeat 1"
   Mismatches
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/db_xref="GI:33786"
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                                                      1 TGTTCTACCACCTGAACTAGGC 22
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1438. .11643
1438. .1488
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/number=2
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nucleic search,

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Run

679419 segs, 1590154680 residues

GenEmbl:\*

1: 9b\_bal:\*

3: 9b\_bal:\*

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em\_hum2:\*
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em\_un: \*
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gb\_htg1: \*
gb\_in1: \*
gb\_in1: \*
em\_ba1: \*
em\_ba2: \*

em\_hum3:\* em\_hum4:\*

gb\_pr4:\*

1 TGTTCTACCACCTGAACTAGGC

IDENTITY\_NUC

Scoring table:

Searched: Database

US-09-037-472-7 22

Title: Perfect score:

Sequence:

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MO0260 E.COLI TTP-
M25066 E.COLI TTP-
M27051 Mycoplasma
X16767 Mycoplasma
AL034390 Leishmani
AL034390 Leishmani
AL034360 Leishmani
D90906 Synechocyst
X72627 Synechocyst
Z67753 O.Sinensis
U73166 Homo sapien
AC005079 Homo sapien
AC005079 Homo sapien
AC005073 Arabidops
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AC005079 Mus muscu
AF03001 Mus muscu
AL049591 Homo sapi
AL049591 Homo sapi
AL049591 Homo sapi
AL049591 Homo sapi
AC00515 Borrelia
AE001155 Borrelia
AF001155 Borrelia
AF013613 Fugu rubr
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X98654 H sapiens m
AC007581 Drosophil
  X03833 Human gene
AL022170 Homo sapi
X14386 Astasia lon
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AF038122 Podospora
AL021155 Homo sapi
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AF106038 Raja radi
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Unknown.
Unclassified.
Unclassified.
I (bases 1 to 22)
Kornman,K.S. and Duff,G.W.
Rornman,K.S. and Duff,G.W.
Detecting genetic predisposition to periodontal disease
Patent: US 5686246-A 1 11-NOV-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 22;
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No. 0.69;
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LMFL684
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SPMULTG
CSCHLPLXX
OSCHLPLXX
AC005085
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AC007323
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HSAC002115
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Sequence 1 from patent US 5686246.
173225
                                            ECOTRW
ECOTRWSUP
MCTRW12
MCTRW2
MYCTGW
MYCTRGC2T
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AE001155
AF028000
GOTMTTGRG
AF013613
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AF106038
  HSILIAG
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                                                                                   September 18, 1999, 15:49:15; Search time 436.05 Seconds (without alignments) 160.456 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
     GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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SUMMARIES

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Ouery Match Length DB

Score

Result No.

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185579 Sequence 2
                                                                   September 18, 1999, 15:49:01; Search time 436.05 Seconds (without alignments) 123.989 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                     679419 seqs, 1590154680 residues
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                                           OM nucleic - nucleic search, using sw model
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BASE COUNT 3 a 4 c 5 g 5 t
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Matches

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DEFINITION ACCESSION HSIL1RECA/c

VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS

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Direct Submission

Submitted (13-JAN-1998) Chromosome 6 Project Group

(http://wwwsanger.ac.uk/HGP/Chr6/) Sanger Centre, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquires:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jan 18, 1998 this sequence version replaced gi:2558561.

IMPORTANT: This sequence is the entire insert of clone 451B15. This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre chromosome 6

mapping group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr6/

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the forter of the forter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     feature key.

The true left end of clone 451B15 is at 1 in this sequence. The true right end of clone 451B15 is at 186510.
451B15 is from the library RPC13 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.

For further details see http://bacpac.med.buffalo.edu/.
                                                                                                                                                                                HS451B15 186510 bp DNA PRI 14-JAN-1998 Human DNA sequence from PAC 451B15 on chromosome 6p24. Contains endothelin, DNA-binding protein, ESTs and STS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3255. 8668

// note="11 repeat: matches 11. 5390 of consensus"
8522. 9408

// note="11PAZ repeat: matches 1. .893 of consensus"
9642. 9776

// note="MIR2 repeat: matches 2. .142 of consensus"
10047. 10345

// note="Alusy repeat: matches 1. .299 of consensus"
15779. 16069

// note="Alusx repeat: matches 20. .302 of consensus"
// note="Alusx repeat: matches 20. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPC13"
complement(222. .774)
/note="match: multiple ESTs; match: AA631424 AA631373"
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/note="LiP848 repeat: matches 695. .909 of consensus" 19153. .20034
/note="LiP841 repeat: matches 900. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186510)
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/hote="AluSq repeat: matches 1. .227 of consensus;
Incomplete repeat"
                                                                                                                                                                                                                                                                                          298050.1 GI:2791272
6P24; DNA-binding protein; EDN1; zinc-finger protein.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p24"
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17752. .17978
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/note="L1MC3
                                                    9279 TCCTGGTCTGCAGGTAA 9263
                             1 TCCTGGTCTGCAGGTAA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-FFB-1992) M.J. Carrier, Yamanouchi Research Institute, Littlemore Hospital, Oxford, Ox4 4XN, UK
2. (bases 1 to 12565)
Lennard, A., Gornan, P., Carrier, M., Griffiths, S., Scotney, H., Sheer, D. and Solari, R.
Cloning and chromosome mapping of the human interleukin-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
    Gaps
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interleukin 1 alpha and beta homologue; interleukin 1 receptor
                                                                                                                                                                                                     25-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mummalia; Eutheria;
Primates: Catarrhin; Hominidae; Homo.
1 (bases 1 to 12565)
Carrier,M.J.
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                                                                                                                                                                              HSILIRECA 12565 bp DNA PRI
H.sapiens gene for interleukin-1 receptor antagonist.
X64532
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/map="q13-14.1"
5949. :5953
5989. :6120
    Indels
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Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 17; Conservative 0; Mismatches
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    Mismatches
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/db_xref="taxon:9606"
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92338323
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9. .6120
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/number=3
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                                         1 TCCTGGTCTGCAGGTAA 17
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11029. .12
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17;
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source

FEATURES

mRNA CDS

JOURNAL MEDLINE

TITLE

intron

intron

exon

intron

exon

exon

BASE COUNT ORIGIN

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Joylou. 20180/

Jotle—"MIR repeat: matches 157. .58 of consensus"

56188. .56323

Jotle—"LIMA4A repeat: matches 1043. .901 of consensus"

56324. .56703

Jotle—"MIR repeat: matches 6. .186 of consensus"

56945. .57025

Jotle—"MIR repeat: matches 66. .186 of consensus"

56953. .57035

Jotle—"AluSx/g repeat: matches 186. .121 of consensus;

Incomplete repeat: matches 51. .1 of consensus;

Incomplete repeat: matches 51. .1 of consensus;

Incomplete repeat: matches 537. .119 of consensus;

57213. .57518

Jotle—"LIMD1 repeat: matches 26. .303 of consensus"

58246. .58154

Jotle—"MER33 repeat: matches 26. .303 of consensus"

58246. .58269

Jotle—"AluSx repeat: matches 1. .302 of consensus"

59200. .58707

Jotle—"AluSx repeat: matches 1. .302 of consensus"

59200. .58707
                                               51118. .51414

Anote-"MSTB repeat: matches 1. .289 of consensus"
51478 .51771

Anote-"Alux repeat: matches 301. .1 of consensus"
51772. .51840

Anote-"LIME3 repeat: matches 335. .403 c. consensus"
53562. .53808

Anote-"LIME3 repeat: matches 296. .551 of consensus"
55194. .55497

Anote-"Aluxo repeat: matches 1. .301 of consensus"
55790. .55887
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/note="MIRZFB repeat: matches 146. .1 of consensus" 63167. .63214
/note="MSTA repeat: matches 376. .423 of consensus" 63247 .63536
/note="MaluSq repeat: matches 301. .10 of consensus" 65081 .65380
/note="MaluSp repeat: matches 1. .301 of consensus" 66041 .66324
/note="MaluSp repeat: matches 1. .301 of consensus" 66041 .66324
                                repeat: matches 589. .866 of consensus"
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/note="MIR2 repeat: matches 144. .41 of consensus" 61162. .61456
/note="Alusx repeat: matches 1. .300 of consensus" 62408. .62451
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8549. 68635
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note="MIR repeat: matches 1. .213 of consensus"
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Pred. No. 31;
0; Mismatches
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100.08;
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TIQSPSSYRLDPAAARHSPOTVAGMENSVASHPHDOPDGKOGVTILQPPEGLESPHTHL
FSHLELHSOQOSRTPYMVPVGGIHVVPAGLTYSTFVPLQAGPVQLTIPAVVYHRTL
GTHRNIVTEVSGTTNPAGVAELSSVVPCIPIGOIRVPGLOLNSTPGLOSLPSLSMETV
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ISVSQVAVDOAGAPEMPSASGSKACETEOPPGOTSVASANQVSTRESPGGLPTVQRENAK
KVLMPPAPAGDHARLDGLSKMOTEKASANHYKPKPELTSIGGPASTSQPLIKAHSE
VFTKPSGQQTLSPDRQVPRPTALPRRQPTVHFSDVSSDDDEDRLVIAT"
                                                                                                                                                                /product="DNA_binding protein"
/protein_id="CAB10847.1"
/db_xref="PID:el237440"
/db_xref="PID:92791274"
/db_xref="FIS:2791274"
/db_xref="GI:2791274"
/db_xref="SPTREMBL:043733"
/translation="DEKQRFSYERSGYDLEESDGPDEDDNENEDDDEDSQAESVLSAT
                                                                                                                                                                                                                                                                                                                                        PSVTASPQHLPSRSSLQDPVSTDEDVRITDCFSGVHTDPMDVLPRALLTRMTVLSTAO
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40120. 40143.

40156. 40163.

40566. 40764. 41213

Anote="hill repeat: matches 5296. 5092 of consensus"
40764. 41213

Anote="hill repeat: matches 45;. 904 of consensus"
40242. 41471

Anote="hill repeat: matches 10. 244 of consensus"
40195. 4018 repeat: matches 3. 124 of consensus;
40195. 40190 repeat: matches 3. 124 of consensus;
40195. 40100 repeat: matches 85. 565 of consensus;
40106-"hill repeat: matches 243. 87 of consensus"
40106-"Aluy repeat: matches 243. 37 of consensus;
40106-"Aluy repeat: matches 2. 301 of consensus;
40106-"Aluy repeat: matches 290. 138 of consensus;
                    /note="L1 repeat: matches 5390. .4746 of consensus"
25324. .28347
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/note="LiMB8 repeat: matches 457. .586 of consensus"
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/note="LiMB7 repeat: matches 30. .547 of consensus"
49993. .50122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32774. .33070
/note="AllSx repeat: matches 302. .3 of consensus"
33746. .34022
31746. repeat: matches 22. .297 of consensus;
incomplete repeat"
35106. .35237
/note="AluJo repeat: matches 133. .1 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anote="16 copies of 2 mer 84 % conserved"
11920. 31999
Anote="40 copies of 2 mer 83 % conserved"
12774. 33070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anote="15 copies of 2 mer 87 % conserved" 31821. 31852 Anote="16 copies of 2 mer 84 % conserved" 31854. 31885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31502. .31558
/note="3 copies of 19 mer 84 % conserved"
31543. .31572. _ -f ? mar 87 % conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 copies of 2 mer 84 % conserved"
31918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        incomplete repeat."
38680. .38706
70ote="9 copies of 3 mer 93 % conserved"
31999. .39348
7note="MIR repeat: matches 96. .255 of cc
                                                              /gene="dJ451B15.2"
join(<25324. .25815,27169. .28347)
/gene="dJ451B15.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31854. .318/note="16 c
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Gaps

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/rpt_type=TANDEM
complement(join(<19155. .19394,20700. .20877,22322. .22476,
33376. .>23450))
'gene="IGF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="G1:2894577"
/translation="METORRAPSECHTCRRTEISIMKVKKMSSSSHALLFALALTL
/translation="METORRAPSECHTCRRTEISIMKVKKMSSSSHALLFALALTL
/translation="METORRAPSECHTCRRTPONACT-PREDECERROP
LKLMEDYCARRAKERENDVANTSLOVIPWRAVKOBYPRKOHYTVKKSKYEWORKAAO
RLRRGVPAILRAKKFRRQAEKIKAQEOTVFHRPLISLPSKLPPVLLTTDSYINHK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(19155. .19394,20700. .20877,22322. .22476,
23376. .23450))
/gene="IGF2"
                           2 (bases 1 to 37170) Dear, S., Dumanski, J., Gibbs, R., Goleman, D., Dear, S., Dumanski, J., Gibbs, R., Goff, S., Heiner, C., Hitte, C., Hoffman, J., James, C., Johnson, D., Khong, N., Kraemer, E., Little, R., Ma, J., McCombie, R., McPherson, J., Muzny, D., Podlutsky, A., Reichard, R., Sandford, R., Schmuck, K., and Zhu, L. 1111, S., Touchman, J., Van Geel, M., Vitale, D., Wilson, R. and Zhu, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="insulin-like growth factor II precursor"
/protein_id="CaAn1123.1"
/db_xref="PID:e1251683"
/db_xref="PID:g2894577"
           Resource Centre, Hinxton, Cambridge, CB10 1SB,
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                                                                                                                                                                                                                               1. .37170
/organism="Fugu rubripes"
/db_xref="taxon:31033"
3194. .3223
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complement(20700. .20877)
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/gene="IGF2"
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                                                                                                                                                                                                                                                                                                                                       /rpt_type=TaNDEM
3400.3488
/note="CA repeat"
/rpt_type=INVERTED
5088.5160
                                                                                                                                                                                                             Location/Qualifiers
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/gene="IGF2"
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/rpt_type=TANDEM
complement(22322.
/gene="IGF2"
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5313. .5329
/note="CA"
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/number=1
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16570. .16654
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10633. .10653
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17454. .17554
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/note="CAG"
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/note="CA"
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/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="CA"
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ALE SUBMISSION

Cambridgeshire, CB10 15A, UK. E-mail enquires:

Cambridgeshire, CB10 15A, UK. E-mail enquires:

Cambridgeshire, CB10 15A, UK. E-mail enquires:

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the contaminated with foreign sequence from E.coli, yeast, vector, phage eas work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished: dJ19F5 Contig_ID: 00179 acc= Length: 1255 bp Unfinished: dJ19F5 Contig_ID: 01378 acc= Length: 1255 bp Unfinished: dJ19F5 Contig_ID: 01204 acc= Length: 6910 bp Unfinished: dJ19F5 Contig_ID: 01204 acc= Length: 6910 bp Unfinished: dJ19F5 Contig_ID: 01204 acc= Length: 1104 bp Unfinished: dJ19F5 Contig_ID: 01204 acc= Length: 1104 bp Unfinished: dJ19F5 Contig_ID: 01205 acc= Length: 16720 bp Unfinished: dJ19F5 Contig_ID: 01205 acc= Length: 16720 bp.

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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0
                         HSDJ19F5 113328 bp DNA HTG 03-JUN-1999
Homo sapiens chromosome 6 clone DJ19F5, WORKING DRAFT SEQUENCE, in
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Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
1 (bases 1 to 37170)
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Submitted (11-FEB-1998) Clark M.S., Fugu Landmark Mapping, MRC-UK
                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 113328)
White, S.
Direct Submission
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Fugu rubripes cosmid 258N02 containing IGFII, TH, NAP2 genes.
AL021880
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Pred. No. 31;
0; Mismatches 0; Indels 0;
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/db_xref="taxon:9606"
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100.0%; Pit
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AL021880.1 GI:2894576
                    113328 bp
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Best Local Similarity 100.
Halches 16: Conservative
                                                                  unordered pieces.
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FR258N02/c
LOCUS
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ACCESSION
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DEFINITION
HSDJ19F5/c
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AUTHORS
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TITLE
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SOURCE
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SOURCE
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Submitted (06-0cT-1998) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Sep 8, 1998 this sequence version replaced gi:3421066.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; neuronal migration protein astrotactin; pregnancy-associated
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Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 121780)
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|Join(<36543. 36352,36516. 36588,36683. >36831)
|Ygene="NAP2"
|36443. 36831
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94.1%; Pred. No. 70;
:ive 0; Mismatches
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                                       complement(27470. .27553)
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/gene="TH"
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complement(27943.
/gene="TH"
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/gene="TH"
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/gene="TH"
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/note="CA"
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                                                                                                             /gene="TH
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Best Local Similarity
Matches 16; Conserv
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VERSION
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                                                  complement(join(<25186. 25345,25675. 25808,25886. 25981,
25359. 26415,26499. 26568,26668. 26803,26614. 27059,
27411. 27471_27472
28323. 28526,28846. >28929))
                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="PID::2894578"
/db_xref="FID::2894578"
/db_xref="GI:2894578"
/translation="MPQSSGSTSSTKSIRRAPSELERSDSVTSQRFLGRRQSLIEDAR
KEREAAAAAEAAAEAAEAAEASEQIVFEEDDOGRALLNIFFTLRNTKTPALSRTLKVFETFEAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HHLETRPCPKIKDSLEGLEYFVRCELHISDVSTLIGSIKRNAEDVKTTKEVKFHWFPK
KIADLDKCHHLVTKFDPDLDQDHPGYTDAAYRQRRKMIGDIAFRYRNGEPIPRVEYTE
EIGTWREVYTULRDLYATHACSEHLEAFRLEAFRCGYSPDNIPQLEDVSCELKEHTG
FILRPVAGLLSARDFLASLFRVFQCTQYIRHASSPHISPEPDCVHELLGHVPMLADS
TFAQFSGSLGLASLGASDEDIEKLSTLYWFYBETGLCKONGEVKAYGAGLLSSYGELV
HSLSDEPEVREFDPDAAAVQPYQDQTYQPVYFISESFADAKERFRYVAGIKRPFSVR
FDPYTTSIQYLDNPKIQGLECVKDELKMLADALSVLS*
                                                                                                                                                                                                                           complement(join(25186. .25345,25675. .25808,25886. .25981,
25359. .26415,26499. .26568,26668. .26603,26914. .27059,
27411. .27471. .27552. .27619,27753. .27841,27943. .28117,
28323. .28526,28846. .28929))
                                                                                                                                                                                                                                                                                                                                  /product="tyrosine 3-monooxygenase"
/protein_id="CAA17124.1"
/db_xref="PID:e1251684"
                                                                                                                                                                         complement(<25186. .25345)
complement(23376, .>23450)
/gene="IGF2"
                                                                                                                                     complement(25186. .28929)
/gene="TH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(25807. .25887)
/gene="TH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(25344. .25676)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(25675. .25808)
/gene="TH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .25981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .26360)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .26803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(26914. .27059)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .26915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(27058. .27422)
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/gene="TH"
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/gene="TH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (26499.
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                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                      /gene="TH"
                                                                                                                                                                                                             /number=13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="TH"
/number=9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="TH
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   exon
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.11881,13959. .14068,20460. .20531,
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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                            neighbouring submissions.

The true left end of clone dJ423N22 is at 121681 in this sequence. This sequence map be finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone 774124. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/HGP/Chrl
774124 is from the library RPC14 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9545. 9955.
/note="L1PA4 repeat: matches 485. 893 of consensus"
join(<10208. 10376,11746. 11881,13959. 14068,20460.
60572. 60670,62779. 66004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4834. .4983)
/note="Mir1A2 repeat: matches 374. .217 of consensus"
complement(4985. .5284)
/note="Mir1A9 repeat: matches 299. .1 of consensus"
complement(5302. .51/6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7231. .7475
/note="LIPA13 repeat: matches 647. .891 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5647. 6943
/note="LIME3 repeat: matches 621. .909 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(11. .230)
//octe="MIR repeat: matches 231. .4 of consensus"
//127. .1170
//note="MIR2 repeat: matches 103. .146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1765. 1796

Anote="16 copies 2 mer tt 100% conserved"

Complement(2154. 2246)

Anote="MER5A repeat: matches 106. 11 of consensus"

2553. 2532. 2832

Anote="MRR repeat: matches 58. .141 of consensus"

complement(2641. .2722)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluSp repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="MIR2 repeat: matches 146. .64 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3536. .3591
/note="MIR repeat: matches 146. .204 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .70 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MLTlal repeat: matches 194. .15 of ocomplement(6429. .6779, /note="match: GSS B76306 clone R-13D11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4228. 4293
/note="MER5B repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(<10208. 10376,11746. 60572. 60670,62779. 62853)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .7934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .121780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="q24.1-24.3"
/clone_lib="RPC14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="dJ774124.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="774124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6647
                                                                                                                                                                                                                                                                                                                                                                                                                                             feature key
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FEATURES

CDS

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/db_xxef-"SPTREMBL:075997"
/translation-"KLLKIQCLEGGIWEQGSCIPVVCEPPPPVFEGWYECTNGFSLDS
/translation-"KLLKIGCLEGGIWEQGSCIPVVCEPPPPPVFEGWYECTNGFSLDS
GCVLNCNOEREKLPILTAFGGLWGFEKLCENLQGECPPPPSELNSVEYKCEQGYGIG
AVCSPLCVIPPSDPWALPENITADTLEHWMEPVKVQSIVCTGRRQWHEDPVLVHCIOS
CEPFQADGWCDTINNRAXCHYDGGDCCSSTLSSKKVIPFAADCDLDECTCRDPKAEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .291 of consensus"
                                                                       to PREGNANCY-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // note="match: GSS AQ018768"
17762. .18057
/note="AluJo repeat: matches 2. .300 of consensus"
/note="LIME1 repeat: matches 430. .518 of consensus"
/note="LIME1 repeat: matches 430. .518 of consensus"
/1056. .21477
/1061. .212133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .893 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="25 copies 2 mer gt 100% conserved"
complement(30731. 31035)
/note="MERIB repeat: matches 336. 35 of consensus"
31062. 31211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14258. .1441/
/note="Alux repeat: matches 46. .206 of consensus"
/note="Alusx/g repeat: matches 252. .291 of consen:
14675. .14800
/note="MIR repeat: matches 99. .234 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // note="17 copies 2 mer ac 97% conserved" 22436. .2280 // note="MERSA repeat: matches 38. .189 of consensus 24376. .24576 // note="MIR repeat: matches 85. .259 of consensus" 24689. .24908 // note="MIR repeat: matches 1. .214 of consensus" 25171. .255610 // gene="dJ774124.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSx repeat: matches 302. .1 of consensus" 3019. .13114
/1001e="LIPA2 repeat: matches 798. .893 of consensu complement(13845. .14115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="16 copies 4 mer cctt 81% conserved"
26100. .26410
7.00te="Allor repeat: matches 1. .302 of consensus"
7.00te="MIR2 repeat: matches 17. .83 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: multiple ESTs; match: H12483 H04693"
25446. .25517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSx repeat: matches 302. .1 of consensus" complement(28588. .28734)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .185 of consensus"
                                                                                                                                                                                                                                                                                                                                                                  11573. .11600
/note="14 copies 2 mer tt 100% conserved"
complement(11947. .12240)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14928. 14961
/note="17 copies 2 mer gt 82% conserved"
15148. 15195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="2 copies 24 mer 100% conserved"
complement(15167. 15835)
/gene="dJ774124.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25446. .25517
/note="3 copies 24 mer 81% conserved"
25449. .25512
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                                      /evidence-not_experimental
/product="dJ774124.1 (similar to
PLASMA PROTEIN A PRECURSOR)"
/protein_id="CAA20358.1"
/db_xref="PID:e1355032"
/db_xref="PID:q3927950"
/db_xref="GI:3927950"
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/note="MIR repeat: matches 62.
complement(27893. .28194)
/note="match: protein 013219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="dJ774I24.1"
/note="match: GSS AQ069552"
/note="match: ARS AQ069552"
/note="match: ARS AQ069552"
                    /codon_start=2
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence may not represent the entire insert of this It may be shorter because we only sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: AL009861 Chromosome 1 HindIII fragment"
41199. .41238
    complement(33181. 34085)

// note="Lizhal2 repeat: matches 911. 1 of consensus"

complement(33940. 35470)

// note="Li repeat: matches 5390. 3854 of consensus"

complement(35944. 36375)

// note="WERAA repeat: matches 661. 229 of consensus"

complement(36372. 36548)

// note="WERAA repeat: matches 173. 1 of consensus"

36549. 36620
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1 (bases 1 to 132953)
Wamsley,P, Kramer,J, Elliott,G and O'Brien,D.
The sequence of H. sapiens BAC clone GS113H23
Uppublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-0CT-1997
/note="MER5A repeat: matches 14. 167 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                      /note="MIR2 repeat: matches 2. .144 of consensus" 40530. 40559
//note="6 copies 5 mer aaaac 93% conserved" complement(40965. 41320)
/gene="dJ774124.1"
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8619. .48678
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Human BAC clone GS113H23 from 5p15.2, complete sequence.
AC003015
                                                                                                                                                                                                                                          /note="34 copies 2 mer ta 90% conserved" 36773. .36810
/note="19 copies 2 mer ca 92% conserved" 28127. .38156
/note="15 copies 2 mer aa 87% conserved" 39389. .39534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="20 copies 2 mer aa 80% conserved" 45085. .45199 /note="MIR repeat: matches 65. .187 of cocomplement(46396. .46552)
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Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
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AC003015.1 GI:2547255
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Best Local Similarity 94.1%;
Matches 16; Conservative
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TITLE
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AUTHORS
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Mapping information for this clone was also provided by Dr. Michael
Lovett, Departments of Otorhinolaryngology, Molecular Biology and
Oncology, University of Texas Southwestern Medical Center, Dallas
                                                                                                                                                                                                                                          Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University School of Medicine, St. Louis MO.
                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is from the first BAC library from Genome Systems, Inc.
clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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complement(6985..7389)
/rpt_family="L1"
complement(7459..8612)
/rpt_family="L1"
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1. .132953
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="L1"
complement(3640, 3667)
/rpt_family="L1"
complement(3764, 3788)
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Cell line: lymphoblastoid
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95. 350
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/map="5p15.2"
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/clone="GS113H23"
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/rpt_family="ALU"
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complement(3820.
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Direct Submission
Submitted (13-JAN-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 13, 1999 this sequence version replaced gi:3907486.
SUBMITTED BY: WUGSC
Genome Sequencing Center
Department of Genetics
Mashington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu 0 Judaces I to 1129483)
Sun,H., Bauer,C., Wohldman,P. and Heidbrink,C.
The sequence of Homo sapiens PAC clone DJ1161G23
Uppublished (1999)
J. (bases 1 to 119483)
Waterston, R. H.
Direct Submission
Direct Submission
University School of Medicine, 4444 Forest Park Parkway, St. Louis, Medicine, 119483)
Waterston,R. H.
Wat NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping Gaps AC005588 119483 bp DNA PRI 13-JAN-1999 Homo sapiens PAC clone DJ1161G23 from 7q36, complete sequence. AC005588 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 119483) Ouery Match 90.6%; Score 15.4; DB 11; Length 132953; Best Local Similarity 94.1%; Pred. No. 70; Matches 16; Conservative 0; Mismatches 1; Indels 0; /rpt\_family="L1" 67996. .68283 /rpt\_family="ALU" complement(68925. .68998) /rpt\_family="L1" 68945. .68993 .64077) .63785) /rpt\_family="L1"
62686.62745
/rpt\_family="L1"
complement(63757
/rpt\_family="L1"
/rpt\_family="L1"
/rpt\_family="L1"
64355.64376 'rpt\_family="ALU" /rpt\_family="ALU" complement(58482. /rpt\_family="ALU" 61733. .62140 /rpt\_family="L1" 58482. .58529 /rpt\_family="L1" complement(59606 /rpt\_family="L1" 70132. .70305 94153863 AC005588.1 GI:4153863 Db 34935 TACTGGTCTGCAGGTAA 34919 1 TCCTGGTCTGCAGGTAA 17 Homo sapiens repeat\_region RESULT 8 AC005588/c LOCUS DEFINITION ACCESSION ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL VERSION KEYWORDS SOURCE COMMENT ô

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17603. 17767 Shotolar dehydrogenase subunit 6 pseudogene; similar to 180240 (PID:g2117562)"
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27137. .27533
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5068. .25091
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!5684. .?san1
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/rpt_family="MIR"
30691. απορο
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19326. 19647
/rpt_family="Alu"
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1389. .21514
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22134. .22441
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0981. .31085
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19842. .19874
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                                                                                                                                                                                  .19813
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                                                                                                                                                                                The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov/ or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                          This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The clone sequenced to the left is DJ1048B16. Actual start of this clone is at base position i or DJ1161G23; actual end is at 119483 of DJ1161G23.
                                                            all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                           This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VECTOR: PCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
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2415..7893
7894..7917
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                                                                                                                                                                    MAPPING INFORMATION:
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/db_xref="PID:q2707375"
/db_xref="AADLETICRPSGRKSSKMQAFRIWDVNQKTFYLRNNQLVAGYLOG
PNVNLEEKIDVVPIEPRALFIGIHGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQD
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join (16201 . 16210, 18246 . 18308, 25876 . 25927, 27756 . 27844,
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X52015 and X53296"
join(25780. .25927,27756. .27844,29053. .29165,30664. .32022)
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join(25812. .25927,27756. .27844,29053. .29165,30664. .30879)
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/translation="MALADLYEEGGGGGGGGGGGGGHADSKETICRPSGFKSSKWQAFRIW
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ETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVS
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x84348"
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                                                                             /product="IL-1 receptor antagonist IL-1Ra, long
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16938. .17227
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 33414)
Jenkins.J.K., Drong.R.F., Shuck,M.E., Bienkowski,M.J.,
Slightom.J.L., Arend,W.P. and Smith,M.F. Jr.
Intracellular IL-1 receptor antagonist promoter: cell type-specific and inducible regulatory regions
J. Immunol. 158 (2), 748-755 (1997)
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Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene,
alternatively spliced forms, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 33414)
Slightom J.L.
Direct Submission
Submitted (30-JUL-1996) Molecular Biology, Pharmacia & Upjohn Company, 301 Hennetti, Kalamazoo, MI 49007, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        Length 119483;
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/rpt_family="(TAAAA)n"
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7note="match to EST T03089 (NID:9314330)"
36105. .36309
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94.1%; Pred. No. 70;
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/Organism="Homo sapiens"
/Organism="Homo sapiens"
/Ob_xref="taxon: 9606"
/Clone="ic-1; P2g"
/Chromosome="l2"
                                                                                                                                                                                                                                                                39727. .40330
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41356. .41531
                                                                                                                     /rpt_family="AT_rich"
38267. .38459
/rpt_family="MaLR"
38470. .38996
                                                                                                                                                                                                 /rpt_family="MER21_g"
39037, .39222
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5614. .5910
/rpt_family="Alu"
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7319. 7590
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/rpt_family="MaLR"
39727. An>..
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/dev_stage="adult"
1. 236
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                                                                               /rpt_family="L2"
37795. .37817
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41563. .41764
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Best Local Similarity 94.1
Matches 16; Conservative
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Direct Submission

Direct Submiston

Cambridgeshire, CB10 18A, UK. E-mail enquires:

Cambridgeshire, CB10 18A, UK. E-mail enquires:

Cambridgeshire, CB10 18A, UK. E-mail enquires:

Indiapportant: Acid Clone requests: clonerequest(sanger.ac.uk

IMPORTANT: This sequence is unfinished and does not necessarily

represent the correct sequence. Work on the sequence is in progress

and the release of this data is based on the understanding that the
contaminated with forteign sequence from E.coli, yeast, vector,

phage etc. Order of segments is not known: 800 n's separate

sequence may change as work conting. Dil. 00859 acc-

Length:

1801 bp Unfinished: dJ106908 Contig_ID: 00859 acc-

Length:

2805 bp Unfinished: dJ106908 Contig_ID: 00803 acc-

Length: 12911 bp

Unfinished: dJ106908 Contig_ID: 0177 acc-

Length: 12911 bp

Unfinished: dJ106908 Contig_ID: 02169 acc-

Length: 12911 bp

Unfinished: dJ106908 Contig_ID: 02169 acc-

Length: 3908 bp

Unfinished: dJ106908 Contig_ID: 02181 acc-

Length: 3908 bp

Unfinished: dJ106908 Contig_ID: 00183 acc-

Length: 3408 bp

Unfinished: dJ106908 Contig_ID: 00184 acc-

Length: 341 bp

Unfinished: dJ106908 Contig_ID: 00554 acc-

Length: 342 bp

Unfinished: dJ106908 Contig_ID: 00554 acc-

Length: 341 bp

Unfinished: dJ106908 Contig_ID: 00554 acc-

Length: 1064 bp

Unfinished: dJ106908 Contig_ID: 00654 acc-

Length: 1064 bp

Unfinished: dJ106908 Contig_ID: 00654 acc-

Length: 1064 bp

Unfinished: dJ106908 Contig_ID: 00484 acc-

Length: 1064 bp

Unfinished: dJ106908 Contig_ID: 00488 acc-

Length: 3418 bp
and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA HTG 10-JUN-1999
20 clone J1069C8, WORKING DRAFT SEQUENCE,
                                                                                           Contigs_order:18a_17_18b; 1000 N's separate segments Contig18a length 5987 bp
Contig17: length 13090 bp.
Contig18b: length 138060 bp.
NOTE: This is a 'working draft' sequence.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 181832)
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/clone_lib="RPCI_11"
31091 c 31465 g 48651 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.4; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
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HTG; HTGS_PHASE1.
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94.1%;
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Direct Submission
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TITLE
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IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress
                       /product="iL-1 receptor antagonist IL-1Ra, secreted form"
//protein_id="AAB92270.1"
//db_xref="PID:92707377"
//db_xref="GI:2707377"
//db_xref="GI:2707377"
//db_xref="GI:2707377"
//db_xref="MEICRGIRSHLITLLLFLFHSETICRPSGRKSSKMQAFRIWDVN OKTFVLRNOLVAFLORPHGERIDVVPTEPHALFLGIHGGKMCLSCVKSGDETR LQLEAVNITDLSENRKODKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADOPVSLIN
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Submitted (14-MAY-1999) Genoscope - Centre national de sequencage
2, rue Gaston Cremieux - BP 191 91006 EVRX cedex - FRANCE (E-mail
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/note="similar to GenBank Accession Numbers X52015 and
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                                                                                                                                                                                                                                                                                                                                                      'note="similar to GenBank Accession Numbers X52015 and
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159137)
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/rpt_family="Alu"
/rpt_type=dispersed
30664. .32022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28708. .28880
/rpt_type=direct
/rpt_unit=28708. .
29053. .29165
                                                                                                                                                                                                    MPDEGVMVTKFYFQEDE"
25928. .27755
/gene="IL-1RN"
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27756. .27844
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/gene="IL-1RN"
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/gene="IL-1RN"
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/gene="IL-1RN"
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AL049873.1 GI:4837625
HTG; HTGS_PHASE2.
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Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
Unpublished
3 (Dases 1 to 91047)
5 (Dases 1 to 91047)
6 Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Maitbie, M., Bussod, M., Sutherland, R., McMurry, K., Han, C. and Deaven, L.
Direct Submission
Nubmitted (06-MAY-1999) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA
* NOTE: This is a "working draft' sequence. It currently consists of 78 contigs. The true order of the pieces stin not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as trus of N but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
* be preserved.
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Homo sapiens chromosome 16 clone 182C10, WORKING DRAFT SEQUENCE, 78
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91047)

Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D.,

Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L.,

Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O.,

Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R.,

Han, C. and Deaven, L.
Unfinished: dJ1069C8 Contig_ID: 01374 acc- Length: 3829 Unfinished: dJ1069C8 Contig_ID: 01572 acc- Length: 1331 * NOTE: This is a 'working draft' sequence. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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94.1%; Pred. No. 70;
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/db_xref="taxon:9606"
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PS 953.793.7 (Constitution) Process 1 to 13143)

Sutton, G.G., Blake, J.A., FitzGerald, L.M., Clayton, R.D., Sutton, G.G., Blake, J.A., FitzGerald, L.M., Clayton, R.A., Gocayne, J.D., Kerlavage, A.R., Dougherty, B.A., Tomb, J., Adams, M.D., Reich, C.I., Overbeek, R., Kirkness, E.F., Weinstock, K.G., Weidman, J.C., Goodyne, J.D., Goodyne, N.S., Weidman, J.F., Fuhrmann, J.L., Nguyen, D.T., Utterback, T., Kelley, J.M., Peterson, J.D., Sadow, P.W., Hanna, M.C., Cotton, M.D., Hurst, M.A., Roberts, K.M., Kaine, B.B., Borodovsky, M., Klenk, H.P., Fraser, C.M., Smith, H.O., Woese, C.R. and Venter, J.C.

Direct Submitsed (27-Aug-1996) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

On Jan 30, 1998 this sequence version replaced gi:1591850.
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S Bult, C.J., White, O., Olsen, G.J., Zhou, L., Fleischmann, R.D.,
Sutton, G. G., Blake, J.A., FlizGerald, L.M., Clayton, R.A.,
Gocayne, J.D., Kerlavage, A.R., Dougherty, B.A., Tomb, J., Adams, M.D.,
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Peterso., J.D., Sadow, P.W., Hanna, M.C., Cotton, M.D., Hurst, M.A.,
Roberts, K.M., Kaine, B.B., Borodovsky, M., Klenk, H.P., Fraser, C.M.,
Smith, H.O., Woese, C.R. and Venter, J.C.
Complete genome sequence of the methanogenic archaeon,
Methanococcus jannaschii
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83433: contig of 2041 bp in length
gap of unknown length
86335: contig of 2902 bp in length
gap of unknown length
91047: contig of 4712 bp in length.
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complement(60. .1796)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus jannaschii section 105 of 150 of 282 of 282 of 3.1 di:2826379
                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                     Score 15.4; DE
Pred. No. 70;
0; Mismatches
                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                         Location/Qualifiers
1. .91047
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Best Local Similarity 94.1%;
Matches 16; Conservative
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DEFINITION
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MEDLINE
REFERENCE
AUTHORS
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KEYWORDS
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VHPIIKFLSYFWNPIAWMIEIAAILSAIIKHWVDFVIILILLLVNGVVGFWEEYKAEN
VIEFLKQKMALNARVLRDGKWQIIPAKELVPGDVVRIRIGDIVPADIILVDGDYLVVD
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YQMIIKIGDYLIVLAVILIAIMVAVBLERGKELIETROFALVLAVSA TAAMMANLS
ITMALGALNIAKKLIAIVKKLVAIERAGUDLCSDKTGTLTKNOLOGEIIAINGFSK
EDVVLFAALASREEDADAIDMAILNEAKKLGLMEKIKNYKIKKFIPFDPVIKRTEAEV
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GIIPLYDPPREDAPLAVKKIKELGVIIKMVTGDHVAIAKNIARMLGIGDKIISISELL
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RILEFVELCILLIGIYPITAAMIVLLAINDPIPLAIAYDPANVEPKSPKRRMERILM
LSTALGLSGVVSEFLIFYISDVELHLTIAELOSFVETRI TLAGHATIFVTRIBDRLWK
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5763. .8180
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complement(4401. .4820)
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ELELYYKAKTWYKITKNVIIKVLLASINGVIGLIEHNIPTLIGAMINAPOLYTSLSS

GTVLGDKELFIQGMKNELLCSGIVIVCAFIPSLFYSKELVLQYLSTSIILSAIVAI

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LLDVGYIGLKYVGKINQKIKY"

complement(2785. 3516)
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PID:535141 percent identity: 31.75; identified by sequence
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                                                                                                                                                                                                                                                                                 RADFSEASYDILGDAYEWILNYFAPTKAKEGEVYTPIEVSKLIAHLVEPKDDEVILDP
ACGSCSMLIEQYRFAGSNPNIVLVGQERNDVTAVLAKLNFILHGINLKDAKVFIGDSL
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/product="M. jannaschii predicted coding region MJ1223*
/protein_id="ABB9235.1"
/db_xref="PlD:g1591854"
/db_xref="G1:1591854"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /hote-"similar to GB:AE000666 percent identity: 44.72; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="hypothetical protein; identified by GeneMark; putative"
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putative"
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/protein_id-"AAB99227 1"
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/transl_table=11
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/gene="MJ1221"
1866. .2765
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/db_xref="PiD: d1040024"
/db_xref="Bi: d521169"
/db_xre
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LNDKVSYPEGTFMDWEFKISVMYDIAKGMSYLHASDIQVHGRLKSTNCVVDNRWVVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Repepterygii; Teleostei; Euteleostei; Acanthopterygii; Atherinomorpha; Cyprinodontiformes; Adrianichthyoidei; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mantoku, T., Muramatsu, R., Nakauchi, M., Yamagami, S., Kusakabe, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mantoku, T., Muramatsu, R., Nakauchi, M., Yamagami, S., Kusakabe, T. and
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Suzuki, N.

Direct Submission

Direct Submission

Submitted (08-70L-1998) to the DDBJ/EMBL/GenBank databases. Norio

Suzuki, Hokkaido University, Division of Biological Sciences,

Graduate School of Science; Kita 10, Nishi 8, Kita-ku, Sapporo,

Hokkaido 060-0810, Japan (E-mail:norio-sesci.hokudai.ac.jp,

Tel:81-11-706-4908, Fax:81-11-746-1512)

On Mar 26, 1999 this sequence version replaced gi:3327368.

Sequence updated (10-Mar-1999).
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the medaka fish homolog of mammalian guanylyl cyclase C
J. Biochem. 125, 476-486 (1999)
2 (bases 1 to 21935)
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11155. 11273,11499. 11601,12024. 12168,13323. 13464,
13548. 13676,14180. 14288,14544. 14625,15278. 15380,
15453. 15509,15591. 15662,15760. 15864,15956. 16042,
17711. 17843,17909. 18046,18115. 18191,18272. 18363,
18444. 18602,19876. 20068,20540. 20714,20786. 20884,
20964. 21058,21132. 21208,21554. 21764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABO16081 21935 bp DNA VRT 16-MAR-1999
Oryzias latipes OlGC6 gene for guanylyl cyclase C, complete cds.
ABO16081
identity: 50.79; identified by sequence similarity;
                                                                                                                                                  ö
                                                               Length 13143;
                                                                       DB 2; Le
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/db_xref="taxon:8090"
6892. .21764
/gene="OlGC6"
                                                                       88.2%; Score 15; DB 100.0%; Pred. No. 1.2 iive 0; Mismatches
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Oryzias latipes DNA.
Oryzias latipes
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                                                                                                                                                                                                                                                                        Db 11795 CTGGTCTGCAGGTAA 11809
                                                                                  Query Match 88.2
Best Local Similarity 100.
Matches 15; Conservative
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Clone requests: clonerequest(sanger.ac.uk
On Aug 21, 1998 this sequence version replaced gi:3280011.
During sequence assembly data is comparated from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

IMPORANAT: This sequence is not the entire insert of clone 1044017. It may be shorter because we arrange for a small overlap between neighbouring submissions.

The true left end of clone 50413 (292545) is at 12226 in this sequence. This sequence has been finished according to sequence map problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu).
Where the sequence is ambiguous, there is an annotation using the
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TDFGCNAFLSREHDLWTAPEHLRKEGTSOKGDVYSFAIICQEIVLRRSTFYTEASLKR
SEKLSRVITSYFRPDLNLETASEKEAEVYMLIKSCWEEDPEKRPDFKKVENLLGKIIS
KIHNODNESYMDNAMRRLOWYSKNIEHLLVEEKTALYKAERDRADRLNFLLPRPVYKS
LKESGAVEPELDBVYTYSDIVGFTTLCOYSTPMEVVDMLNDIYKGFDSIVDHHDVY
KVETIGDAYMVASGLPNRNGNMHAVDICRMALDILEFWGTFQLRHLVGIPVWIRIGVH
SGPCAAGVVGVKMRYKCLFGDTVNTASRMESTGHPLR.HVSEPTIQILQRTNCKFEYE
MRGETYLKGKGTEMTYWLTGESGQDYDLPPTTENVORLQOHLAHMILACLERRSRG
SYRRKKQHADOGKNDBDEBSGVVESESSQPEYLHLATVDNTLSTFL"

4588 c 4625 g 6515 t
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Submitted (09-OCT-1998) E-mail enquiries: humquery@sanger.ac.uk
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.2%; Score 15; DB 4; Le 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0;
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/db_xref="taxon:9506"
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/clone_lib="RPC15"
382. .2592
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AL023875.1 GI:3449106
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Best Local Similarity
Matches 15; Conserv
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.*"L1 repeat: .2815 .*"14 copies :	eat: ma	5 to 5	. ä	۰ دة	ote. 30.	 				/note="L1PA7 repeat: matches 516890 of consensus" 12081, .14318	/note="L1 repeat: matches 30605390 of consensus" 14201 15013	/note="Limbar repeat: matches 30872 of consensus" complement(1605) 16359.	: :	matc	·	0110)	marches 235 388 of consensus		matches 402453 of consens: 3391)	mat 1058	E .:	/note="L1 repeat: matches 38984474 of consensus" 24600 24811	7,000- 124011 /note=MLT1G repeat: matches 18233 of consensus" 2495, 25073	Inote="MITIF repeat: matches 380529 of consensus"	Comprement(20072: .2073) /note="MIR repeat: matches 22141 of consensus" 27606 38049	7.000 "Solves" for matches 1424 of consensus" 20330 20642	E 5	atc natc	- 1	/note="MSTA repeat: matches 1426 of consensus" 32748 33119	/note="MER25 repeat: matches 17122086 of consensus" 33716 33503	/note="L1 repeat: matches 16951988 of consensus" 33770 34487		. " 2 E	ָ עַב.	repeat: ma
peat_regio	eat_regio	pear_reg	eat_regio	= ´ eat_regio	eat regio	eat regio	eat regio	pat regio	eat_regio	at_region	pat region	eat region	to de la contraction de la con		c o	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	at region	neat region	eat region	reaction reaction	doings + eac	at region	100,000,000	t region	at redi	at regi	at regio	at redi	at regi	at region	at region	160110000

Autonome ment (4339). Another say (339) of consensus (3554-1188) repeat: matches 675. 539 of consensus (4532-4188) repeat: matches 675. 539 of consensus (4532-4188) repeat: matches 673. 922 of consensus (4532-4470) rote="MLTIG repeat: matches 1. 186 of consensus" (4600. 45088 repeat: matches 1. 186 of consensus (4600. 45088 repeat: matches 69. 541 of consensus (4600. 45088 repeat: matches 69. 541 of consensus (4600-45088 repeat: matches 69. 541 of consensus (4600-45088 repeat: matches 69. 541 of consensus (4601-4612 repeat: matches 184. 102 of consensus (4601-4612 repeat: matches 184. 102 of consensus (4601-4612 repeat: matches 184. 102 of consensus (4601-4613) repeat: matches 184. 102 of consensus (4601-4613) repeat: matches 182. 262 of consensus (4601-4614) repeat: matches 182. 262 of consensus (4601-4614) repeat: matches 182. 364 of consensus (4601-4614) repeat: matches 661. 495 of consensus (4601-4614) repeat: matches 28. 460 of consensus (4601-4614) repeat: matches 814. 104 of Complement(39599. 40328)

Complement(39599. 40328)

Complement(39599. 40328)

Complement(39599. 40328)

Complement(39599. 40328)

Anote-"L1 repeat: matches 1294. 631 of consensus."

A1281. 44417

A1281. 44417

Anote-"L1MA2 repeat: matches 919. 1055 of consensus."

A127. 4216

A127. 4216

A127. 4284

Anote-"L1 repeat: matches 11. 299 of consensus."

A1281. 42891

Anote-"L1 repeat: matches 2906. 3339 of consensus."

A1281. 42891

Anote-"L1 repeat: matches 3479. 3945 of consensus."

A2999. 43377

Anote-"L1 repeat: matches 3479. 3945 of consensus."

A2999. 43377

Anote-"L1 repeat: matches 3479. 3945 of consensus."

Complement(43397. 43536) Comprement() 1972... 1970.)

/ Note="MSTA repeat: matches 310. .1 of consensus" 54889... 55140

/ Note="MIR repeat: matches 2. .261 of consensus" complement(55862... 55914)

/ Note="MLTIF repeat: matches 517... 464 of consensus" 57446... 57479

/ Note="17 copies 2 mer ca 88% conserved" 57483... 57522

/ Note="12 copies 2 mer ga 90% conserved" 58284... 58487

/ Note="11 repeat: matches 1761... 1981 of consensus" complement (36013. repeat\_region misc\_feature misc\_feature misc\_feature

Search completed: September 18, 1999, 15:49:15 Job time: 1435 sec

Mycobacteriophage

76.5 52297 1 T51411

13

44

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic - nucleic search, using sw model
..... Oli: September 18, 1999, 05:27:21; Search time 213.04 Seconds
(without alignments)
19.965 Million cell updates/sec

Title: US-09-037-472-6
Perfect score: 17
Sequence: 1 TCCTGGTCTGCAGGTAA 17

Scoring table: IDENTITY\_NUC

Searched: 311585 seqs, 125096042 residues

Database : N\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	tion	uman	IL-1RN gen	erleukin-1	primer used	receptor	interleukin	7	tion (3 o	Suc	gment	ch cyste	SHOC-1 CDN	ıtınase	eum Cycl	Human EHOC-1/ prot	nterococcus t	H	Human aspartoacyla	ector	1-4 he	heavy cha	ρrostat	1/gamma	1/gamma1	1/gamma1	/gamma1	n kidney a	DNA CO	Ĕ	įq	Human secreted pro	ጟ	HIV-1-NC infection	ucleot	repres	Plasmid pUR3001 ,	D-amino-acid-oxida	uman brain	L5 mycobacteriopha	edneuce eu	rebellar á	Chicken oocyte rec	tie-2 recep
SUMMARIES		1 6	4	53	V60231	23	23	5622	7	۱	004735	4 7	9	ή.	2 (	אַכּ	ဘ္က	8	4	55	7	72	5	25	ß	5	V65982	35	79	21	<b>4</b> 3	9	51	σ	05	39	14	0	059458	73	26	47	49	93
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	ALLGNMENIS	
RESULT 1 T89948		
ID T89948 stand	standard; DNA; 17 BP.	
DT 05-MAR-1998	(first entry)	(
KW Interleukin	redain'i receptor antagonist ill'ira; ulcerative co	litis;
KW diagnosis;	prognosis; inflammatory bowel disease; PCR pi	imer; ss.
OS Homo sapien	.51	
PN W09725445-2	11.	
PD 17-JUL-1997		
PR 12-JAN-1996	; U00042. ; US-587911.	
PA (CEDA-) CEL	DARS SINAI MEDICAL CENT.	
PA (UYVI-) UNI	V VIRGINIA PATENT FOUND.	
DR WPI; 97-372	7, Fizarro 1, notice 31, rang n, 1880/34.	
PT Screening 1	for ulcerative colitis in subjects of Jewish	ncestry - by
PT detecting a	MITELS 2 OF the VNIK (Variable number of tands om at intron 2 of the IL-1 receptor antagonis	n repears)
PS Claim 7; Pa	ige 17; 22pp; English.	)
CC PCR primers	: T89947 and T89948 are used to amplify intro	2 of the
CC to screen i	icanin i receptor antayonist yene (in ina) in or ulcerative colitis (UC) in a subject of Ju	wish ancestry.
CC There is ar	association between allele 2 of the variable	number of tandem
CC repeats (V)	VTR) polymorphism at intron 2 of IL-1ra, an in regulator of inflammation, and NC in humans	portant f Jewish
CC ancestry. 1	his method can be used for the diagnosis and	prognosis of UC
CC and other i	ic in Jewish patients for UC and distinguishing UC from Crohn's disease (CD) ic and other inflammatory disease of the bowel.	nn's disease (CL
SQ Sequence	17 BP; 3 A; 4 C; 5 G; 5 T;	
Query Match Best Local Sin Matches 17;	h Similarity 100.0%; Pred. No. 3.4; 17; Conservative 0; Mismatches 0; Indels	7; 0; Gaps
f	r- ** = 50 * 00 = 0 = 0	
OP 1 TCCTGC	TCTGGTCTGCAGGTAA 1/ 	
RESULT 2		
103410 ID T89410 star	standard; cDNA; 17 BP.	
AC T89410;	, first 054 mil	
DE Human IL-1	42 AFR 1990 (1115) entry) Human IL-1RN gene intron 2 PCR primer 2.	
KW Osteoporosi	antagonist; I	allele;
OS Synthetic.	it density; post-menopause; rok primer; ss.	
OS Homo sapier	18.	
PD 16-0CT-1997		
PF 03-APR-1997 PR 05-APR-1996	7; U05626. 5: US-628282.	
PA (MEDI-) MEI	(MEDI-) MEDICAL SCI SYSTEMS INC.	
DR WPI; 97-512	2741/47.	
PT Detecting of	osteoporosis - by	detecting
		;
	ed to amplify a	on of the
	1-1 re eptor antagonist gene, IL-1RN, intron 2	which

## (first entry)
used to amplify interleukin-1 receptor antagonist (IL-1RN).

V60231 standard; DNA; 17 BP.

RESULT V66231

25-NOV-1998 PCR primer

Interleukin-1 receptor antagonist, IL-1RN; predisposition; coronary artery disease; screen; PCR primer; ss.

17-SEP-1998. 09-MAR-1998; U04725. 10-MAR-1997; US-813456. (MEDI-) MEDICAL SCI SYSTEMS INC. Crossman DC, Duff GW, Francis SE; WPI; 98-520829/44.

WO9840517-A1.

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Symptomic occur.

Claim 2: Page 33: 41pp; English.

Claim 2: Page 31pp; English.

Claim 3: Page 31pp; English.

Claim 4: Page 31pp; English.

Claim 5: Page 31pp; English.

Clai
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a variable number tandem repeat (VNTR) region that gives rise to five allelles. This product is used for predicting the risk of osteoporosis in subject by determining the allelic and genetic polymorphism pattern for IL-1RN in genomic DNA. A pattern of at least one copy of the IL-1RN allele 2 indicates an increased susceptibility to osteoporosis. The methods can predict low bone mineral density (BMD) and the rate of bone density loss and thereby a susceptibility to osteoporosis. Individuals so identified can then be treated more aggressively to prevent or retard the occurrence of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin-IRN primer 2.
Genetic polymorphism. PCR; primer; amplification; interleukin-IRN;
sight threatening diabetic retinopathy; interleukin-1-alpha; IL-IRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Predicting increased risk of sight-threatening diabetic retinopathy comprises identifying genetic polymorphism pattern for genes IL-IA, IL-IB and IL-IRN, useful to allow treatment before clinical
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                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 17; DB 1; Lergth 17; 100.0%; Pred. No. 3.4;
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G;
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C;
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09-OCT-1997; G02790.

10-OCT-1996; GB-021129.

(DUFF) DUFF G.

(RENN/) RENNIE I.

(RICH/) RICHARDSON R.

(DUFF G. Rennie I. Richardson R;

WPI; 98-240835/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V32394 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                        3 A;
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Best Local Similarity 100.
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WO9815653-A1.
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Comparative measurement of levels of expression of alleles from the
Interletkin 1 locus
Claim 6: Page 15: 22pp; English.
Claim 6: Page 15: 22pp; English.
Claim 6: Page 15: 22pp; English.
Claim 6: Page 16: 22pp; English.
Claim 7: Page 16:
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A method has been developed for the diagnosis of osteoporosis comprising determining the genotype of an interleukin-1 (IL-1) receptor antagonist gene (IL-IRN). The present sequence represents a PCR primer adapted to amplify a portion of introm 2 of an IL-IRN for use in the method of the invention. The method can be used for the diagnosis of disease, including diagnosis of osteoporosis and predisposition or susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL-1 receptor antagonist gene intron 2 PCR primer #2.
Human; interleukin-1 receptor antagonist gene; IL-1; polymorphism;
diagnosis; osteoporosis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosis of osteoporosis by determining genotype of interleukin-1 receptor antagonist gene - useful for diagnosing patient pre-disposition or susceptibility to osteoporosis and for
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Pred. No. 3.4;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.
Matches 17; Conservative
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27-MAR-1998; G00944.
27-MAR-1997; GB-006359.
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98-557135/47.
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WO9844150-A1.
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Best Local Similarity

Query Match Matches

1 TCCTGGTCTGCAGGTAA 17 1 TCCTGGTCTGCAGGTAA 17 17; Conservative

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100.0%; Score 17; DB 1; Length 17; 100.0%; Pred. No. 3.4;

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Disclosure: Page 21-27; 36pp; English.
A method has been developed for the diagnosis of osteoporosis comprising
determining the genotype of an interleukin-1 (IL-1) receptor antagonist
gene (IL-1RN). The present sequence represents the human interleukin-1
gene (IL-1RN). The present sequence represents the human interleukin-1
disease, including diagnosis of osteoporosis and predisposition or
susceptibility to osteoporosis and for therapy.
Sequence 1256, BP; 3217 A; 2980 C; 3072 G; 3294 T;
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Interleukin 1 (44112332) haplotype PCR primer #16.
Interleukin 1; IL-1; haplotype; inflammatory disorder; alopecia areata; coronary artery disease; osteoporosis; nephropathy; diabetes mellitus; Graves disease; systemic lupus erythamatosus; lichen sclerosis; ulcerative colitis; PCR primer; ss.
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V62392.C
ID V63392.C
ID
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29-MAY-1997; GB-011040.
(CAMP/) CAMP N J.
(COXA) COX A.
(DGIO/) DE GIOVINE F S.
(DUFF/) DUFF G.
CAMP NJ, COX A, De Giovine FS, Duff G;
                                                         ΰ
to osteoporosis and for therapy
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                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
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Matches 17; Conserv
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Homo sapiens.
WO9854359-A1.
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                                                                 Seguence
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V21209 from base 200001 (Methanococcus jannaschii circular fragments LOCUS V21209 Accession V21209
While you would your the presence of an IL-1 (44112332)

The processors of proteins produced by the IL-1 gene cluster

Claim 3; Page 33; 49pp. English.

Comparison of proteins produced by the IL-1 gene cluster

Claim 3; Page 33; 49pp. English.

Comparison of an inflammatory disorder. The method comprises the detection of an interleukin 1 (IL-1) (44112332) haplotype in a sample obtained from the classorder. Xi6607 to Xi6631 represent PCR primer used in the method for detecting the IL-1 (44112332) haplotype. The method provides kits for the early prediction of a patient's susceptibility to an inflammatory content of a patient's susceptibility to inflammatory disorders, including coronary artery disease, osteoporosis, nephropathy aloabetes mellitus, alopecia areata, Graves diseases, systemic lupus contents, comparising diabetic retinopathy, juvenile chronic arthritis, alobetes mellitus, alopecia areata, Graves diseases, systemic lupus contents, comprising diabetic retinopathy, juvenile chronic arthritis, disease-associated haplotype can be applied to particular inflammatory disease-associated haplotype enables determination of which alleles are causative, and this information is useful in designing treatment contents. Comparising gene therapy and treatment using various agents that modulate the activity of proteins produced by the IL-1 gene cluster contrally in the pathology of these diseases. Therefore, the use of IL-1 contrally in the pathology of these diseases. Therefore, the use of IL-1 diffammatory diseases, including those with a molivenic component contrally in the pathology of these sets diseases. Therefore is to long with a molivenic component.
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Mismatches
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710000
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100.08; F1.
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200001
300001
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V21209_02/c
Continuation (3 of 17) of V2
WP Sequence split into 17 fr
WP Sequence split into 17 fr
WP V21209_01
WP V21209_02
WP V21209_03
WP V21209_03
WP V21209_04
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WP V21209_11
110
WP V21209_13
WP V21209_13
WP V21209_14
140
WP V21209_16
150
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Best Local Similarity
Matches 17; Conserv
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12-JUN-1995 (first entry)
Spinach cysteine synthase.
Cysteine; spinach; spinacia oleracea; pUC19; M13mp18; plant; nutrition; feed value; pharmaceutical; food additive; cosmetic; E.coli; ds.
Spinacia oleracea.
                                                                                                                                                            is useful for expression of human alpha-2 plasmin inhibitor, etc.
                                                            12-0cT-1990 (first entry)
Gene fragment encoding human alpha-2 plasmin inhibitor.
Alpha-2 plasmin; alpha-2-PI; ds.
                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a /product= cysteine synthetase
                                                                                                                                                                                                          Score 14.4; Di
Pred. No. 84;
O; Mismatches
                                                                                                                                                                                                                                                                                                           Q74413 standard; cDNA to mRNA; 1483 BP
                                                                                                                                                                               360 C;
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1993; JP-038527.
(MITS) MITSUBISHI CORP.
(MITU) MITSUBISHI KASEI CORP.
WPI; 94.32128/740.
P-PSDB; R63756.
                                            Q04735 standard; DNA; 1226 BP
                                                                                                                                                                               188 A;
                                                                                                                                                                                                          84.7%;
93.8%;
                                                                                                                                                                                                                                                      246 CCTGGTCTGCAGGTCA 261
                                                                                                                                                                                                          Query Match 84.7
Best Local Similarity 93.8
Matches 15; Conservative
246 CCTGGTCTGCAGGTCA 261
                                                                                                                                                                                                                                              2 CCTGGTCTGCAGGTAA 17
                                                                                                                                                                      Disclosure; p; Japanese.
Sequence 1226 BP; 18
                                                                                                                31-OCT-1988; 272903.
31-OCT-1988; JP-272903.
                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-1994.
26-FEB-1993; 038527.
                                                                                                                                   (TEIJ) Teijin KK.
WPI; 90-182383/24.
Gene fragment -
                                                                                        Homo sapiens.
J02119782-A.
                                                                                                           7-MAY-1990
                         RESULT 10
Q04735
                                                                                                                                                                                                                                                                                          RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human alpha-2-plasmin inhibitor protein coding gene has specified exons bonded to each other via intron. Claim 1: Page 451: 10pp: Japanese Claim 1: Page 451: 10pp: Japanese Protein is derived from 10 exons of the gene widely spaced by introns up to 6.0kb in length. When inserted into a suitable expression vector host animal cells can be used to produce human alpha-2-plasmin inhibitor, useful in diagnosis and therapy of the plasmin inhibitor defficiency disease. Sequence 6306 BP: 1146 A: 1861 C: 1961 G: 1338 T:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 6306;
                                    13.5EP-1990 (first entry)
Sequence encoding human alpha-2-plasmin inhibitor.
Alpha-2-plasmin; alpha-2-plasmin inhibitor deficiency
disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.4; DE
Pred. No. 89;
0; Mismatches
                                                                                        Location/Qualifiers
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4316.
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,9. .4641
/*tag= 0
4642.
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/*tag= p
4753.
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                             Q04100 standard; DNA; 6306 BP
                                                                                                                                                                               881. .899

/*tag= a

900. .1936

/*tag= b

1937. .2003

/*tag= c
                                                                                                                                                                                                           2268. .2330
/*tag= 9
/*tag= 9
2641. .2842
/*tag= 1
2843. .3821
/*tag= 3
3822. .3965
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4753. 4957
/*tag= q
4754. 5137
/*tag= 5547
/*tag= s
                                                                                                                                                     2004. .2108
/*tag= d
2109. .2147
/*tag= e
2148. .2267
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Best Local Similarity 93.8
Matches 15; Conservative
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21-SEP-1988; JP-234930
21-SEP-1988; JP-234930
(TELJ) Teijin KK.
WPI; 90-137117/18.
P-PSDB; R04252.
                                                                                   Homo sapiens
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              RESULT
004100
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Gaps

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1; Indels

Length 1226;

DB 1;

260 T;

418 G;

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                                                                                                                                          The nucleotide sequence of the novel cysteine synthase enzyme from The nucleotide sequence of the novel cysteine synthase enzyme from a papinach, Spinacia oleracea. The probes (07414-5) were used to obtain a clone from a cDNA library derived from spinach seedling leaves. The 1.5 kb insert was ligated into the cloning vectors pUC19 and M13mp18. The gene, 1483 bp, encodes a protein of 383 a.a. The cysteine gene is expressed in plants to elevate the cysteine content in the plant. The nutritional and feed value of the plant are expected to be enriched. Cysteine, one of the 5-containing amino acids, can be used as materials for various pharmaceuticals, food additives or cosmetics. Production of the protein is a useful step in the production of cysteine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Gene encoding a cysteine synthesis enzyme - useful for elevating cysteine content in plant bodies increasing their nutritional
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0
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2 CCTGGTCTGCAGGTAA 17

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Gaps

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1; Indels

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Rowe

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Chitin biosynthetic enzymes end I, exo I and exo II - are periplasmic chito:dextrinase(s), periplasmic beta-GlcNAcidase(s) and aryl beta-N-acetyl:qluco:amidase(s), respectively Example 4; Page 78-79; IOIPp; English. Periplasmic chitodextrinase (W02156), periplasmic chitodextrinase (W02156), periplasmic beta-N-acetylglucosaminidase (W02158) and aryl beta-N-acetylglucosaminidase (W02158) can be used to produce chitin oligosaccharides with the structure (GlcNAc)n where n is 2 or higher, by contacting them with soluble chitin. The enzymes are encoded by the genes end!, exoI and exxII respectively. They are all genes involved in the catabolic pathway of chitin. Sequence 2951 BP; 629 A; 960 C; 880 G; 482 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6: Page 17-41; 93pp; English.
This sequence encodes an enzyme which has cyclosporin synthetase-like activity. This sequence was isolated from Tolypocladium niveum (formerly known as T. inflatum GAMS). The enzyme encoded by this sequence catalyses the peptide biosynthesis of cyclosporins and structurally related molecules. This sequence may be used for the production of cyclosporin by transforming a vector containing this sequence in to a recombinant host. This allows effective production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T. niveum Cyclosporin synthetase gene.
Enzyme; cyclosporin; synthetase-like activity; Tolypocladium niveum;
T. inflatum GAMS; biosynthesis; vector; cyclosporin synthetase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated DNA sequence - which codes for enzyme having cyclosporin synthetase like activity
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29-APR-1993; CH-001310.
04-MAY-1993; CH-001375.
(SANO ) SANDOZ LTD.
(SANO ) SANDOZ PATENY GMBH.
(SANO ) SANDOZ PATENY GMBH.
Leitner E, Schneider E, Schoergendorfer K, Weber G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= Cyclosporin synthetase 40239. .43129
                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                           ś
                                             Roseman
                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.4; I
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
13-FEB-1995; US-386727.
(UVJO ) UNIV JOHNS HOPKINS.
Bassler B, Chitlaru E, Keyhani N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment, Claim 4"
37781. .40244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment, Claim 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O54386 standard; DNA; 46899 BP
                                                                                                                                                                                                                                                                                                                                                                                                       84.78;
93.88;
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/*tag= a
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            989 TCCAGGTCTGCAGGTA 974
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05-JUL-1993; 810474.
09-JUL-1992; AT-001403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tolypocladium niveum.
                                                                              WPI; 96-393335/39.
P-PSDB; W02159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 94-010432/02.
P-PSDB; R44929.
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Q54386
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Soluble chitinase coding sequence (chiA gene).
Periplasmic chitodextrinase; periplasmic Beta-N-acetylglucosaminidase;
Beta-N-acetylglucosamidase; chitin; oligosaccharide; catabolic;
catabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    locus 922.3

Claim 5; Page 39 45; 62pp; English.

The human EHOC-1 gene (T29600) is derived from the q22.3 locus of chromosome 21, which is the site of mutations that cause progressive myoclonus epilepsy of the Unverricht Lundborg type (EPM1), autoimmune polyglandular disease type I (APECED) and holoprosencephaly (HPE1). It was obtd. by construction of a bacterial artificial chromosome contig of a EPM1-APECED-HPE1 candidate region and use of a direct CDNA selection technique. The gene can be used for prodn. of EHOC-1 polypeptide (R95241), to design diagnostic probes and primers, to supply wild-type gene function to a mutated EHOC-1 gene, to design antisense sequences for therapeutic appln., and to breed transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human EHOC-1 gene, chromosome 21 gene marker - useful to prepare probes for detection of mutation(s) and aneuploidies in chromosome
                                                                                                                                                                                                              Human EHOC-1. cbMA.
EHOC-1. chromosome 21. gene marker; genome; mutation; aneuploidy;
progressive myoclonus epilepsy; PME; homoprosencephaly; HPE1;
autoimmune polyglandular disease type I; APECED; artisense;
gene therapy; diagnosis; transgenic animal; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1324 G;
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Pred. No. 88;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= Soluble chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1322 C;
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
138. .3710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-1994; US-337690.
(CEDA-) CEDARS SINAI MEDICAL CENT.
Korenberg JR, Yamakawa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1237 A;
                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/label= EHOC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T36390/c
TD T36390 standard; DNA; 2951 BP.
                                                                                                                                        T29600/c
ID T29600 standard; cDNA; 5107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.7%;
93.8%;
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                                                                                                                                                                                                  (first entry)
                                         839 CCTGGTGTGCAGGTAA 854
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                    2 CCTGGTCTGCAGGTAA 17
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13-FEB-1996; U02332.
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Best Local Similarity
Matches 15; Conserv
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WPI; 96-259777/26.
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Length 2951;

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A cDNA clone (766902) codes for novel human EHOC-17 protein (18197), an acceptionline-activated cationic channel permeable to ca2+ ions. A cDNA library from a 14-wk trisomy 21 foetal brain was screened with bacterial artificial chromosomes covering the 21922.3 cregion. Specifically bound material was amplified by PCR and used to probe the cDNA library, yielding the EHOC-17 clone. The clone maps proximal to D21525, i.e. within the consensus region for the maps proximal to D21525, i.e. within the consensus region for the conspirated in progressive myoclonal epilepsy, autoimmune polyglandular disease type I and holoprosencepha!y. A transcript of the EHOC-17 gene is expressed in a wide range of adult tissues. EHOC-17 oligonucleotides can be used to detect mutations and aneuploidies at 21922.3, while entisense oligonucleotides can be used to modulate expression of EHOC-17 polypeptide. Cells cape to modulate expression of EHOC-17 polypeptide. Cells cape to modulate expression of EHOC-17 polypeptide. Cells cytential therapeutic agents. Transgenic animals can be used to setuence 3125 BP; 688 A; 845 C; 928 G; 664 T;
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                                                                                                                   Gaps
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                10226 T;
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                                                                       82.4%; Score 14; DB 1; Length 46899; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
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10-001.1997 (first entry)
Human EHOC-17 protein cDNA clone.
EHOC-17; progressive myoclonus epicepsy: holoprosencephaly:
autoimmune polyglandular disease type i; transgenic animal;
chromosome 21; ion channel; ss.
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                12509 G;
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100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0;
of antibiotic cyclosporin or its derivatives. Sequence 46899 BP; 10651 A; 13513 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
25. .2784
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1995; US-006453.
07-NOV-1996; US-006453.
(CEDA-) CEDARS SINAI MEDICAL CENT.
KOTENDERG JR, YAMARAWA K;
                                                                                                                                                                                                                                                                                                   T66902 standard; cDNA; 3125 BP.
                                                                                                                                                                               Db 20672 TCCTGGTCTGCAGG 20685
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Matches 14; Conservative
                                                                           Query Match 82.4 Best Local Similarity 100. Matches 14; Conservative
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08-NOV-1996; U17989.
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T66902
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23.867 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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H09124 y197h05.51
RS5963 yhl1a03.51
W26640 34b6 Human
AA038299 m183403.51
AA155819 ZX47C02.r
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AA35783 ZF57C08.r
AA310957 EST182660
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A17073 UI-R-Y0-m
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A1585162 fb95a08.y
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A1045952 Homo sapi
T16114 IB3506 Infa
H52729 yo34a11.s1
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AA22733
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bp mRNA EST 24-NOV-1998 2NbMT Mus musculus cDNA clone IMAGE:1395175 5',

AI286716 490 ub84d04.rl Soares

LOCUS DEFINITION

RESULT AI286716

GI:3926469

mRNA sequence. AI286716 g3926469 AI286716.1 GI:

ACCESSION NID VERSION

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Query Match
Best Local Similarity
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        ORGANISM
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                                                                                                Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIS85162 695 bp mRNA EST 06-APR-1999 fb95a08.yl Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to gb:J03464 PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN); contains PTR5.t3 PTR5 repetitive element; , mRNA sequence.
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                                                                                                                                                                                                                                                                        Washugton University School of MedicineP
Washigton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:906891
Seq Primer: -28813 rev2 ET from Amersham
                                                   Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                        Unpublished (1996)
On Dec 5, 1997 this sequence version replaced gi:2662843.
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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/Clone_lib-"Soares 2NbMT"
//sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 426. Location/Qualifiers 1. 490 /organism="Mus musculus" /db_xrei="taxon:10090" /map="19"
                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
                                                                                                                                                                                        The WashU-HHMI Mouse EST Project
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94.18;
                                   Mus musculus
Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                     (bases 1 to 490)
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes: Cyprinoidea; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 695)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Rddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,P., Harvey,N., Schurk,R., Waterston,R. and Wilson,R.

Washu Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                          Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
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                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
                                                                                                                                                                                                                                                                    On Jun 5, 1998 this sequence version replaced gi:3186954
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Seq primer: T3 ET from Amersham
High quality sequence stop: 479.
Location/Qualifiers
1. 695
/organism="Danio rerio"
/db_xref="taxon:7955"
/db_xref="taxon:7955"
/clone_lib="Zebrafish WashU MPIMG EST"
/sex="mixed"
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94.1%; Pred. No. 1.2e+02;
Live 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                         Contact: Stephen L. Johnson
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(jboothr@popserver.stanford.edu)
Seq primer: T3
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100.0%; Pre
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/db_xref="taxon:7955"
/dbocxref="taxon:7955"
/dbocxref="taxon:7955"
/dev_stage="embryonic day 3 post-fertilization"
/dab_host="E.coli XLI-Blue mrF"
/dab_host="E.coli XLI-Blue mrF"
/note="Organ: heart; Vector: Lambda ZAP Express; Site_1:
ECORI; Site_2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. ECORI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
                                                                                                                                                         Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
1 (bases 1 to 406)
Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and
                                                                                                                                                                                                                                                                                  Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3188789.
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                  AI616774 406 bp mRNA EST 21-APR-1999 zehn0590.seg.F Zebrafish Embryon.c Heart CDNA Library Danio rerio
                                                                                                                                                                                                                                                                                                                                                                       Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Invitute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Fax: 4169788550
Email: liewcc@utc.utoronto.ca
PCR PRimers
FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CAAGGGAATTGTAATACCACTCACTAAAGGG 3'
Seq primer: 5' GAAAATTAAACCCTCACTAAAGGG 3'
Location/Qualifiers
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Eukaryota: Alveolata: Apicomplexa: Coccidia: Eimeriida;
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94.1%; Pred. No. 1.1e+02;
1ve 0; Mismatches 1;
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1 (bases 1 to 419)
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102 c 13
                                                   CDNA 5', mRNA sequence.
                                                                                          94625941
AI616774.1 GI:4625941
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Matches 16; Conserv
                                                                                                                                            zebrafish.
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1 (bases 1 to 593)

1 (bases 1 to 593)

Kyushiki, H., Nagara, M., Hishigaki, H., Horie, M., Kawai, A., Kuga, Y., Kyushiki, H., Nagara, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Suzuki, M., Takaichi, A., Takeda, S., Watanabe, T., Maekwa, H., Nakamura, Y. and Takahashi, E.

Otsuka cDNA project
Unpublished (1996)

On Sep 12, 1996 this sequence version replaced gi:1393845.
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C18373 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone
GEN-561C11 5', mRNA sequence.
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Hehl,A., Manger,I., Marra,M., Sibley,L.D., Ajioka,J.A., Aslett,M.A., Dierrich,N., Dubuque,T., Hillier,L., Kucaba,T., Wan,K.L., Waterston,R.H. and Boothroyd,J.
WashU-Merck-Stanford-NIH Toxoplasma EST project Unpublished (1996)
On Apr 14, 1993 this sequence version replaced g1:693311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washur Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fmax: 314 286 1810
Email: toxo@watson.wustl.edu
Clones are available from Genome Systems (genome@MO.NET);
library is available from John Boothroyd
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Pred. No. 1.9e+02;
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Location/Qualifiers
1. 419
/organism="Toxoplasma gon/strain="ME49, clone PDS"
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human.
                                                                                                                                                                                                                                                       Query Match
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DEFINITION
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JOURNAL
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H09134 'c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA193570 379 bp mRNA EST 14-FEB-1997 zr42a04.sl Soares_NhHMPu_Sl Homo sapiens cDNA clone IMAGE:666030 3'similar to contains element L1 repetitive element ;, mRNA sequence.
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             Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463:10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tal: 0886-52-2888
Fax: 0886-37-1035.
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/dbc="IMAGE:666030"
/clone="Inb="Soares_NhiMFu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: mixed (see below); Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40Ml3 fwd. from Amersham High quality sequence stop: 292.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 379)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Socres,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
On Nov 29, 1993 this sequence version replaced gi:501856
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19p12-p13.1"
/clone="dEN-561C11"
/clone=lib="Human placenta cDNA (TFujiwara)"
/tissue_type="placenta"
a 122 c 163 g 137 t 2 others
                                                                                                                                                                                                                                                                                                                                                                          88.2%; Score 15; DB 28; Length 593; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
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/organism="Homo sapiens"
/db_xref="GDB:5428062"
                                                                                                                  Location/Qualifiers
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Tsutomu Fujiwara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA193570.1 GI:1782971
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Matches 15; Conserv
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normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. Clones 260232-265223, 340488-345479, and 484488-489479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
Insert Size: 1594
Insert Size: 1594
Insert Size: 1594
Insert Size: 1594
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: Promega - 21m13
High quality sequence stop: 362.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 468)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H09124 468 bp mRNA EST 23-JUN-199
y197h05.s1 Soares infant brain 1NIB Homo sapiens cDNA clone
IMAGE:46496 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
On May 5, 1995 this sequence version replaced gi:797863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                     Length 379;
                                                                                                                                                                                                                                                                                                                                                                     Indels
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/Organism="Homo sapiens"
/db_xref="CDB:419077"
/db_xref="taxon:9606"
/clone="IMAGE:46496"
/clone=lib="Soares infant brain INIB"
                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                   88.2%; Score 15; DB 29; 100.0%; Pred. No. 1.8e+02;
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H09124.1 GI:873946
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les 15; Conserv
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Gaps

; 0

Indels

Length 445;

us-09-037-472-6.rst

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Email: est@watson.wustl.edu
High quality sequence stops: 296
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: SP6
High quality sequence stop: 296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 498)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebratu; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                     K59693 498 bp mRNA EST 24-MAY-199
yhlla03.sl Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:42773 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washingto: University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                Score 14.4; DB 22;
Pred. No. 3.9e+02;
0; Mismatches 1;
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                                                              84.78;
93.88;
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R59693.1 GI:830388
                                                                                                                                                             384 TCCTGGTCCGCAGGTA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
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Fax: 314 286 1810
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Matches 15; Conser
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                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800

Fax: 314 286 1810

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1709

High quality sequence stops: 365 Source: IXAGE Consortium, LLNL

This clone is available royalty free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: MI3RPI

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases I to 445)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                        RS9129 445 bp mRNA EST 24-MAY-199
yg96c09.rl Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:41341 5', mRNA sequence.
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Unpublished (1995)
On May 8, 1995 this sequence version replaced gi:800177
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                       Length 468
                                                                                                                                                                                          Indels
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/clone_lib="Soares infant brain 1NIB"
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                                                                                                                                                   Score 14.4; DB 2
Pred. No. 4e+02;
); Mismatches
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/db_xref="GDB:413882"
/db_xref="taxon:9606"
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93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        R59129.1 GI:829824
                                                                                                                                                                                                                                               320 TCCTAGTCTGCAGGTA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                        15; Conservative
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Matches 15; Conserv
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R59129/c
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                                                                                      Length 498;
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                                                                                    84.7%; Score 14.4; DB 22;
93.8%; Pred. No. 4e+02;
live 0; Mismatches 1;
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ĀA038299.1 GI:1513706
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93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 93.8
Matches 15, Conservative
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AA125309
g1684541
AA125309.1 GI:
EST.
                                                                                                   Mus musculus
                                                            EST.
house mouse.
  AA038299
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                                                                                                 ORGANISM
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AA125309
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COMMENT
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ORIGIN
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                                                                                                                                                           REFERENCE
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KEYWORDS -
SOURCE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="Human retina cDNA randomly primed sublibrary"
/sex="mixed (males and females)"
/dev_stage="retina"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="E. coli strain K802"
/note="Organ: eye; Vector: lambda gtl0; Site_1: EcoRI;
Site_2: EcoRI; The library used for sequencing was a sublibrary derived from a human retina cDNA library.
Inserts from retina cDNA library DN, were isolated, randomly primed, PCR amplified, Size-selected, and cloned into lambda gtl0. Individual plaques were arrayed and used as templates for PCR amplification, and these PCR products were used for sequencing."
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                                                                                                                                                W26640 917 bp mRNA EST 08-MAY-1996
34b6 Human retina cDNA randomly primed sublibrary Homo sapiens
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 917)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Dr. Jeremy Nathans
Dr. Jaremy Nathans,
Dyn Brens, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
Tel: 410 955 4678
Fax: 410 614 0827
Email: jeremy_nathans@qmail.bs.jhu.edu
                                                                                                                                                                                                                                                                                                                                                                                      Macke, J., Smallwood, P. and Nathans, J.
Adult Human Retina CDNA
Unpublished (1996)
On May 18, 1995 this sequence version replaced gi:811365.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: CTTTTGACCAAGTTCAGCCTGGTTAAGT
BACKWARD: GAGGTGGCTTATGAGTATTTCTTCCAGGGTAA
Seg primer: GGGTAAAAAGCAAAAGAATT.
Location/Qualifiers
                                                                                                                                                                                                      W26640
91307483
W26640.1 GI:1307483
                                                                                                                                                                                        cDNA, mRNA sequence.
                                 321 TCCTAGTCTGCAGGTA 306
          1 TCCTGGTCTGCAGGTA 16
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                                                                                                                                                                                                                                                                                                              Homo sapiens
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Matches 15; Conser
                                                                                                                                                                                                                                                                                           human.
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 576)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R., and Waterston,R.
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                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:283933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                  Unpublished (1996)
On Sep 21, 1992 this sequence version replaced gi:279401
                                                                                                                                                                                                                                                                                          Washu'HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mul:20355
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 417.
Location/Qualifiers
                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
                                                                                                                                                                           The Washu-HHMI Mouse EST Project
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tags

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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AA227533 288 bp mRNA EST 24-FEB-1997
25, mRNA sequence. hHMPU_S1 Homo sapiens CDNA clone IMAGE:667502
AA227533
                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 396.
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1 (bases 1 to 288)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                 Generation and analysis of 280,000 human expressed sequence Generation Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson,R.
The MasMu-Merck EST Project
Unpublished (1995)
On Sep 12, 1996 this sequence version replaced gi:1392732.
                                                                                                                                                                                                                                                                                                                                        On Sep 12, 1996 this sequence version replaced gi:1309494
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Pred. No. 4.1e+02;
0; Mismatches 1;
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AA227533.1 GI:1849159
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93.8%;
(bases 1 to 583)
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Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
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AA227533/c
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AUTHORS
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//dev_zstage="4 weeks"
//dev_zstage="7 weeks"

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                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 634)
Marray M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                        The WashD-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1282806.
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 634;
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93.8%; Pred. No. 4.2e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 308.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:575042"
/clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .634
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA155819.1 GI:1727496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                        Waterston, R.
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Matches 15; Conserv
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source

FEATURES

RESULT 13
AA155819/c
LOCUS
DEFINITION

ACCESSION

VERSION

42

g ò

BASE COUNT ORIGIN

KEYWORDS SOURCE ORGANISM

; 0

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pregnant uterus"

[lab_host="DH10B"

[lab_host="DH10B"

[Anote="Organ: mixed (see below); Vector: pT7T3D-Pac

[Anote="Organ: mixed (see below); Vector: pT7T3D-Pac

[Anote="Organ: mixed (see below); Vector: pT7T3D-Pac

[Anote="Organ: mixed mounts of plasmid DNA from three normalized libraries (melanocyte 2NbHW, pregnant uterus

NDHPU, and fetal heart NDHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223,

340488-345479, and 484488-489479."
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                                                                                                                                                                                                                                                      1. 288
/organism="Homo sapiens"
/db_xref="GDB:5561469"
/db_xref="taxon:9606"
/clone="INAGE:667502"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                              Tel: 314 286 1810

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 407)
Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter, Rapid CDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain CDNA library
Nature Genet. 4, 373-380 (1993)
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On May 8, 1995 this sequence version replaced gi:801297
Other_ESTs: EST12914 THC173606
Contact: Kerlavage, AR
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.4; DB 30; Length 288;
Pred. No. 3.6e+02;
0; Mismatches 1; Indels 0
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Email: arkerlav@tigr.org
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AA303078.1 GI:1955408
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For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi.html) Seq primer: M13-21.
                                                                               Gaps
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Pred. No. 3.9e+02;
0; Mismatches 1;
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Job time: 3660 sec
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Matches 15; Conservative
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AF011366 Xiphophor AF011386 Xiphophor AF011395 Poecilia J00898 chicken ovo V00441 Chicken ovo X18159 Glycine max AC003028 Arabidops D86982 Human mRNA AJC254041 Homo Sapi AL023580 Human DNA S 297353 Human DNA S 289031 Human DNA S
                                  X64532 H.sapiens g
U65590 Homo sapien
AF031389 Poecilia
AE000669 Aquifex a
AE000763 Aquifex a
U86689 Erwinia chr
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AF031387 Poecilia
AF031389 Poecilia
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AF031400 Poecilia
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Neopterygii: Teleostei: Euteleostei; Acanthopterygii;
Atherinomorpha: Cyprinodontiformes; Cyprinodontoidei; Poeciliidae;
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AC005261 Homo sapi
AC006154 Homo sapi
AF015720 Homo sapi
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Poecilia perugiae NADH dehydrogenase subunit 2 gene, mitochondrial gene encoding mitochondrial protein, complete cds.
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Breden,F., Ptacek,M., Rashed,M., Taphorn,D. and de Figueiredo,C.A.
Molecular phylogeny of a live-bearing fish genus Poecilia
(Cyprinidontiformes: Poeciliidae) based on NAbH dehydrogenase subunit 2 sequence variation
                 AF084973 Heterandr
185578 Sequence 1
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Breden,F., Ptacek,M. and Rahsed,M.
Direct Submission
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HS695020B
HS695020
AHU14748
AF031386
AF031395
CHKOVMZ
GGOVOZ
GGOVOZ
ATMCOM328
ATMCOM328
BMSSLWSRP
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HSU65590
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AE031388

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123.989 Million cell updates/sec
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                                                               September 18, 1999, 15:48:58; Search time 436.05 Seconds
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          GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                        679419 segs, 1590154680 residues
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                                              OM nucleic - nucleic search, using sw model
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AWGOHPPRAYDETTYTYPRAGARSATLLEAGISORAFILGEWDILHTPYTSTSTLITLAL
AMKIGLAPLHSWMPEWGGLNLLTGIILSTWOKLAPLYLIYOIOPNSPHTFILGLLS
IIVGGWGGFNOVOLRKILAYSSIAHLGWMILLISFSPPLALLTITLIYLLMTFSLFSLF
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LATRATHINSLSTWAKIPILYYYTHLASIGGLPPLXGFNFWLILOELTKODLAP
LATLAALSSEFSLYFYTRLSYAMTLSMPPNNPAGTLPWRLNPOHNFLMALTTSTIC
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Mitochondrion Poecilia reticulata
Mitochondrion Poecilia reticulata
Bukaryota: Metazoa; Chordata: Craniata; Vertebrata; Actinopterygii;
Bukaryotii: Teleostei: Euteleostei; Acanthopterygii;
Atherinomorpha: Cyprinodontiformes; Cyprinodontoidei; Poeciliidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF031393 1105 bp DNA VRT 30-NOV-1997
Poecilia reticulata NADH dehydrogenase subunit 2 gene,
mitochondrial gene encoding mitochondrial protein, complete cds.
   Sciences, Simon Fraser
Burnaby, BC V5A 1S6, Canada
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Breden,F., Ptacek,M. and Rahsed,M.
Direct Submission
Submitted (27-OTT-1997) Biological Sciences, Simon Fraser
University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada
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/note="Tribe Poeciliini; Oropuche River, Oropuche
Drainage, Trinidad"
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/transl_table=1
/product="NADH dehydrogenase subunit 2"
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/protein_id="AAB87617.1"
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ive 0; Mismatches 0;
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Submitted (27-OCT-1997) Biological
University, 8888 University Drive,
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IATLAALSSLFSLYFYRLBYAMTLTMPRNNPAGTLPWRLNPTHLMSLATTSTIC
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ILTRATHINSLSTWAKIPILTISTPLILLSFGGLPPLTGFWFWLILQELYGOLTP
LATLAALSSESLYFYLRLSYAMTLTWSPNNPAGTLPWRLNPPLMALTTTSTIC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
Atherinomorpha; Cyprinodontiformes; Cyprinodontoidei; Poeciliidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1997
mitochondrial
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Breden,F., Ptacek,M. and Rahsed,M.
Direct Submission
Submitted (27-OCT-1997) Biological Sciences, Simon Fraser
University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada
1 - 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                               4; Length 1105;
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/note="Tribe Poeciliini; Georgetown,
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Pred. No. 15;
Mismatches
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/mitochondrion
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Best Local Similarity 100.0%;
Matches 17; Conservative 0
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Score 17; DB 4; Length 1105;

100.08;

Gaps

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/db_xref="G1:33799"
/db_xref="G1:33799"
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Submitted (17-FEB-1992) M.J. Carrier, Yamanouchi Research
Institute, Littlemore Hospital, Oxford, OX4 4XN, UK
2 (bases 1 to 12565)
Lennard, A., Gorman, P., Carrier, M., Griffiths, S., Scotney, H., Sheer, D. and Solari, R.
Cloning and chromosome mapping of the human interleukin-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(5989. .6120,7952. .8040,9418. .9530,11029.
join(6005. .6120,7952. .8040,9418. .9530,11029.
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/db_xref="PID:933799"
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X64532
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
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26;
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interleukin 1 alpha and beta homologue;
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1 (bases 1 to 12565)
Carrier,M.J.
                                                                                                                                                      Unclassified.

(bases 1 to 17)

Duff,G.W., Russell,G. and Eastell,R.

Detecting genetic predisposition for Patent: US 5698399-A 1 16-DEC-1997;
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5949. .5953
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Pred. No. 2

    12565
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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Cytokine 4 (2), 83-89 (1992)
92338323
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Best Local Similarity 100.
Matches 17; Conservative
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TITLE
JOURNAL
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MILRTHISSISTTWAKIPALTASVPLILLSGLGGLPPTGFLPRWLILDELTKONLTL
IALSAALSSLFSLYFYLRLSYAMALTMPPNNPGTLPWRLSSNNNTTIFALTGATIL
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bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
Atherinomorpha; Cyprinodontiformes; Cyprinodontoidei; Poeciliidae;
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mitochondrial gene encoding mitochondrial protein, complete cds.
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(Cyprinodontiformes: Poeciliidae)
(Cyprinodontiformes: Poeciliidae)
(Cyprinodontiformes: Fool: (1999) In press
2 (bases 1 to 1105)
Breden, F., Ptacek, M.B., Rashed, M. and de Figueiredo, C.A.
Direct Submission
Submitted (21-AUG-1998) Biological Sciences, Simon Fraser University, Burnaby, BC V5A 156, Canada
Location/Qualifiers
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/country="USA:South Carolina, Savannah River"
<33. >1079
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1 (bases 1 to 1105)
Breden,F., Ptacek,M.B., Rashed,M., Taphorn,D. and de
Figueiredo,C.A.
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33. .1079
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/transl_table=2
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/protein_id="AAD27788.1"
/db_xref="PID:g4689159"
/db_xref="G1:4689159"
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/mitochondrion
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Sequence 1 from patent US 5698399.
  Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                   join(16201. .16210,25876. .25927,27756. .27844,29053. .29165,
30664. .30879)
/gene="IL-IRN"
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join(25812. .25927,27756. .27844,29053. .29165,30664. .30879)
/gene="IL-1RN"
       .18308,25876. .25927,27756. .27844,
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                                                                                                           /product="IL-1 receptor antagonist IL-1Ra, long intracellular form"
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/gene="iL-1RN"
/note="intron 1 of short intracellular form"
16211. .18245
/gene="iL-1RN"
/note="intron ic1"
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join(16075. .16210,18246. .1:
29053. .29165,30664. .32022)
/gene="IL-1RN"
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/rpt_type=dispersed
23996. 24284
/rpt_family="Alu"
/rpt_fype=dispersed
25780. 25927
/gene="IL-1RN"
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18246..18308
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/gene-"IL-1RN"
16075. .16210
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/gene="IL-1RN"
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join(16075. 16210,25876. .25927,27756. .27844,29053. .29165,
30664. .32022)
/gene="IL-1RN"
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 33414)
Jenkins.J.K., Drong.R.F., Shuck,M.E., Bienkowski,M.J.,
Slightom.J.L., Arend.W.P. and Smith,M.F. Jr.
Intracellular IL-1 receptor antagonist promoter: cell type-specific and inducible requiatory regions
J. Immunol. 158 (2), 748-755 (1997)
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Submitted (30-JUL-1996) Molecular Biology, Pharmacia & Upjohn
Company, 301 Hennretti, Kalamazco, MI 49007, USA
Location/Qualifiers
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5614. .5910
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   MPDEGVMVTKFYFQEDE'
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8041. .941
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Hypothetical indicates similarity to a protein of unknown function.
Location/Qualifiers
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Aquifex aeolicus
Bacteria: Aquificales; Aquificaceae; Aquifex.
1 (bases I to 1277)
Deckert,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L., Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M., Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V. The complete genome of the hyperthermophilic bacterium Aquifex
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                                        Sciences, Simon Fraser
Burnaby, BC V5A 1S6, Canada
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Submitted (25-JUL-1997) Diversa Corporation, Genomics,
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/organism="Poecilia latipinna"
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100.0%; Pred. No. ...
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  Direct Submission
Submitted (27-OCT-1997) Biological
University, 8888 University Drive,
Location/Qualiflers
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33. .1079
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AE000669 AE000657
q2982762
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    . 2100
    /gene="fusA"
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Best Local Similarity 100.
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LQLEAVNITDLSENFKQD: FAFTRSDSGPTTSFESAACPGWFLCTAMEADQPVSLTN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
Atherinomorpha; Cyprinodontiformes; Cyprinodontoidei; Poeciliidae;
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                                                                                                                                                                                                                                                                                                                    /note="similar to GenBank Accession Numbers X52015 and
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Pred. No. 9.9;
0; Mismatches 0; Indels 0:
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Poecilia latipinna NADH dehydrogenase subunit 2 ge
gene encoding mitochondrial protein, complete cds.
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/rpt_unit=28708. .29794
29053. .29165
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Breden, F., Ptacek, M. and Rahsed, M.
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30664. .32022
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27756. .27844
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25928. .27755
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Matches 17; Conservative 0;
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Gaps

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LSDKARNALIFVDNUDLGKKRRYRKAIEFLKNLGVBREKVLVVIPERADVLYKSFRN
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/gene="rplB"
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kakcekyeeidkapeekergitinithveyetakrhyahvdcpghadyiknmitgaaq
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Pelmpi Edvesisgrotvytgrvergvlkpgdbvejvglrebelkyrsieberky
Dealpgdnigvllrgvgkddvergvlargesvkahkreraqvyvlskeeggrhtpfy
vnyrpofyfrtadvytglybeggvenwpgdnveleveliapvaleeglrfrirgg
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DLNSRRGKIMGMENKGVITVIKAHVPLAEMFGYATTLRSLTQGRGTFIMKFSHYDEVP
QQIAEKIIGERMAGKSS"
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3346 3660
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CDS

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FASATAVLLRIMDVPTRLVSGFYGANKNEYGNYYIVINAMAHVWVEAYDGKKWVRVDT
TPPYVPEGVREVSKLALFYDALITFWYNNVVNFNTQKQRKVFTDTVKTVKTLLBEIKE
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EIAEELGDKVKVGKLNTDENPNIAMRYGIRAIPTIILFKNGEVVDTRIGVQPKERLNK
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SEIKRIQLRESVRWKVKLPVKFTLLKENGEEINAEGQLEDISVKGARVCFEGRLDIKE
GDRILLDFTLKNYTFKNLLGTVVHQIVYEKRTCLGIKFEELSRKEEEVIGGFILEEGR
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KYLKEEKVETVEEGIKVAFIGRPNVGKSSLVNAILKDERVISYSPAGTTRAJEIPFR
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              SWFFFVILPRANQPLFDLFSQKKAGLISGISEEVELGKVGEIQLDRTVVLRVFGLEFK
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PLRVVIPAFWVSELKTAFEIVFLLVIPFLIVDLVVASILISMGIIMIPPQLISLPFKI
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3387. .4688
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/gene="era2"
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SVVEVRVPELDAQLVAQDIATQIERRVSHRRAMKRAIDNALKAGAKGVKVQVKGRIGG
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                                                                                                                                                                                           /translation="MGQKTHPIGFRLGVIKEWPSKWYAPKKEYSKLLHEDLKIKNYIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative indicates no similarity to known proteins
Hypothetical indicates similarity to a protein of unknown function.
Location Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-JUL-1997) Diversa Corporation, Genomics, San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deckett,G., Warren,P.V., Gaasterland,T., Young,W.G., Lenox,A.L., Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M., Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V. The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deckert.G., Warren.P.V., Gaasterland,T., Young,W.G., Lenox,A.L., Graham,D.E., Overbeek,R., Snead,M.A., Keller,M., Aujay,M., Huber,R., Feldman,R.A., Short,J.M., Olson,G.J. and Swanson,R.V. Direct Submission
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Pred. No. 86;
0; Mismatches 1; Indels 0;
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1 (bases 1 to 11891)
                                                                                             /product="ribosomal protein S03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Aquifex aeolicus"/strain="VF5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative protein"
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219. .1676
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                                                                                                                                                                                                                                                                                                                              /joce="aq_018"
8017. 8445
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                                              /codon_start=1
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219. 1676
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/gene="rplP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.6%;
94.1%;
7317. .7955
/gene="rpsC
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Best Local Similarity 94.1
Matches 16; Conservative
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Aquifex aeolicus
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/db_xref="G1:1794194"
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Submitted (11-SEP-1995) Biological Sciences, Texas Tech University,
Flint and Main, Lubbock, TX 79400-3131, USA
On May 14, 1999 this sequence version replaced gi:2429101.
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Valmeekam, V., Freeman, T.L., Loh, Y.-L. and San Francisco, M.J.D.
Regulation of galacturonate transport in Erwinia chrysanthemi EC16
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECU86689 3360 bp DNA BCT 17-MAY-1999
Erwinia chrysanthemi exuT (exuT) and exuR (exuR) genes, complete
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The exuT gene of Erwinia chrysanthemi EC16: nucleotide sequence, expression, localization, and relevance of the gene product Mol. Plant Microbe Interact. 11 (4), 270-276 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 11891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                   /anticodon=pos:10052. .10054,aa:Gly)
10124. .10196
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10282. .11499
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10019. .10091
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                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.4; DE
Pred. No. 87;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                    /note="aq_1928"
10282. .11499
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296. .1333
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                                                                                                                                                                                                                                                                                                                                                                                                                      90.68;
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Best Local Similarity
Matches 16; Conserv
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INNYRAITLSAVYAVISLLGSDIPVNEGGPRPLEVITRKGSVVDAREPPAGYAGGNVE
TORTUDVVLGAFSKAIPEKVPAASOGTMNHVYIGGINPENGEPFTYETIGGGMAS
AKGDGESAVHSHMYNTLINPIEALEHYYPILVTEYSIRKGSGGGGMIRGGDGIVREYE
FLTDVEVTVLSERRRLAPYGLFGGKPGMPGINLIKTEBGEKEMPSKFSVYLKKGDRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MKKALGILAILLIUVGGYFAYDKYMDNKAKEQVEYFLDKTLRKS
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VKGKGLLEEYGYKDPKFNLFVGYFEAKPKEFFHLRSLSLDYPBAFEVNISFILGNYDH
AFWKTVALSDRPPERSVSFQYLSELGSIKINSLEVYRDKGFKERVIKKEAQKRGKTPE
EFKKELIRKIEEEKLKARSEFERNLLDAFEKFLEKGKEITVV
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PEKENLVAPOAAHIVYHLGSWPLSVKEATKAFKGEFEBCDWVVLNDPYMGGTHLDDIT
LVAPFFYKGELLFFARRAHADVGATPGSMPLSVFIPGEFIIPPLKLAMKRGELNE
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TVIAPDGDLKLGEDVVYVLIKGKEDEERAAKYPPNVKVIVETTDWTVIPLENLIAQRE
ELYAVVKNAQEAEVALQTLEKGVKGVVLKSRDINEIKKVGQIVSEHEEKLELVTIKIT
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LGISVKQSPSEEKRKGKIPK KELKEKENPPIOVDVSYTPPETGTDRVALAXSAKKFYGKN
VVVISAGTALVIDLVLEGKEKGGFTTLGLGKKLKILSDLAEGIPEFFPEEVEFLGRS
TRECVLGGAYRESTEFIKSTLKMRKVFKRKFKVVITGGEGKYFSKFGIYDPLLVHRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KILPLGLGDRVCVDTISLLHRGEGMLVGNSSGGMFLVHAETEENPYVAARPFRVNAGA
VHMYIRVPNNRTKYLCELKAGDKVMVYDYKGRGRVTYVGRAKVERRPMLLIEGRYENK
KLSCILQNAETIRLTKPDGTPISVSELKEGDEVLGYVEEAGRHFGMKVEETIIEK"
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9925. .10009
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                                                                                                                                                               /codon_start=1
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LLPMTPAIMALLPF"
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Mitochondrion Poecilia gilli
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Actinopterygii;
Neopterygii: Teleostei: Euteleostei; Acanthopterygii;
Atherinomorpha: Cyprinodontiformes; Cyprinodontoidei; Poeciliidae;
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Breden, F., Ptacek, M., Rashed, M., Taphorn, D. and de Figueiredo, C.A. Molecular phylogeny of a live-bearing fish genus Poecilia (Cyprinidontiformes: Poeciliidae) based on NADH dehydrogenase subunit 2 sequence variation
                                                                                                                                                                                                                                                                                                                                                                                                                                      AF031388 1105 bp DNA VRT 30-NOV-1997 Poecilia gilli NADH dehydrogenase subunit 2 gene, mitochondrial gene encoding mitochondrial protein, complete cds.
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Direct Submission
Submitted (27-00T-1997) Biological Sciences, Simon Fraser
University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada
Location/Qualifiers
                                                                                                                                                                                                                     Length 1105;
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Pred. No. 1.2e+02;
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94.1%; Pred. No. 1.2e+02;
live 0; Mismatches 1;
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ALDTSPCFVR"
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Mitochondrion Poecilia vivipara
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
Atherinomorpha; Cyprinodontiformes; Cyprinodontoidei; Poeciliidae;
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Poecilia vivipara NADH dehydrogenase subunit 2 gene, mitochondrial
gene encoding mitochondrial protein, complete cds.
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Breden, F., Ptacek, M., Rashed, M., Taphorn, D. and de Figueiredo, C.A. Molecular phylogeny of a live-bearing fish genus Poecilia (Cyprinidontiformes: Poecilidae) based on NADH dehydrogenase
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Burnaby, BC V5A 1S6, Canada
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917 c 879 g 753 t
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Pred. No. 1e+02;
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Breden,F., Ptacek,M. and Rahsed,M.
Direct Submission
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Mitochondrion Poecilia sphenops
Eukaryota: Metazoa: Chordata: Craniata: Vertekrata; Actinopterygii;
Neopterygii; Teleostei: Euteleostei: Acanthopterygii;
Atherinomorpha; Cyprinodontiformes; Cyprinodor.toidei; Poeciliidae;
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Poecilia sphenops NADH dehydrogenase subunit 2 gene, mitochondrial
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Breden, F., Ptacek, M., Rashed, M., Taphorn, D. and de Figueiredo, C.A. Molecular phylogeny of a live-bearing fish genus Poecilia (Cyprinidontiformes: Poeciliidae) based on NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF031394 1105 bp DNA VRT 30-NOV-1997 Poecilia reticulata NADH dehydrogenase subunit 2 gene, mitochondrial gene encoding mitochondrial protein, complete cds.
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Breden,F., Ptacek,M. and Rahsed,M.
Direct Submission
Submitted (27-OCT-1997) Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada Location/Qualifiers
1. 1105
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels 0
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/note="Tribe Poeciliini"
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Unpublished
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Matches 16; Conservative
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Mitochondrion Poecilia reticulata
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei: Euteleostei; Acanthopterygii;
Atherinomorpha; Cyprinodontiformes; Cyprinodontoidei; Poeciliidae;
Poecilia.
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TIGGWGGROVQLKRILTAYSSIAHLGYMLLLILSFAPPLALITILIYLLMFFSLESSF
MLTRTTHINGLATTWAKIPILTISTPLYLLSGLGGLPPLTGFWRWLILDELTKODLAP
IATLAALSSLFSLYFYLRLSYAMTLTMPPNNPAGTLPWRLNTRHNTTMASLTTTSTIC
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Breden, F., Ptacek, M., Rashed, M., Taphorn, D. and de Figueiredo, C.A.
Molecular phylogeny of a live-bearing fish genus Poecilia
(Cyprinidontiformes: Poeciliidae) based on NADH dehydrogenase
subunit 2 sequence variation
                                                                                                                                                                                                                                                                                    2 (bases 1 to 1105)
Breden, F., Ptacek, M. and Rahsed, M.
Briect Submission
Submitted (27-OCT-1997) Biological Sciences, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:8081"
/note="Tribe Poecilini; Aripo River, Caroni Drainage.
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Poecilia reticulata"/mitochondrion
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Job time: 1421 sec
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94.1%;
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Best Local Similarity 94.1
Matches 16; Conservative
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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0; Search time 213.04 Seconds (without alignments)
19.965 Million cell updates/sec September 18, 1999, 05:27:20 - nucleic search, using sw model nucleic Run on: ŏ

US-09-037-472-5 17 1 CTCAGCAACACTCCTAT 17 Title: Perfect score: Sequence:

IDENTITY\_NUC Scoring table: 311585 seqs, 125096042 residues Searched:

N\_Geneseq\_36:\* Database Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	% Query Match	% Ouery Match Length DB	DB	DI	Description
1				:		
H	17	100.0	17	-	T89947	Human Interleuki
7	17	100.0	17	Н	T89409	Human IL-1RN gen
٣	17	100.0	17	-	V32393	Interleukin-1RN
4	17	100.0	17	-	V60230	PCR primer used
2	17	100.0	17	Н	V62390	IL-1 receptor an
9	17	100.0	12565	Н	V62392	Human interleuki
7	17	100.0	17	-4	X16621	Interleukin 1 (4
80	14.4	84.7	369	Н	T72131	CEA-specific ant
6	14.4	84.7	786	Н	X05452	CEA6 antibody si
10	14	82.4	2481	٦	V40019	Mouse Pax6 gene.
11	14	82.4	2481	7	V40035	Mouse Pax6 gene
c 12	14	82.4	2245	٦	V61485	Human secreted p
13	14	82.4	3597	Н	V81414	Human prenylcyst
c 14	14	82.4	2084	٦	X37379	Human secreted p
c 15	14	82.4	2078	٦	X37439	Human secreted p
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	T89947	940	39	023	239	39	662	7213	545	001	003	148	141	7	43	36	96	Н	14	<b>*</b>	1	1	411	17	12	12	~	12	12	12	26	58	V65381	38	94	181	023	578	374	T94534	591	9	92
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0.0	78.8	
13.4	13.4	
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## ALIGNMENTS

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PF 17-JUL-1997; U00042.

PR 12-JAN-1997; U00042.

PR 12-JAN-1997; U00042.

PR 12-JAN-1996; US-587911.

PA (CEDA-) CEDARS SIMIA MEDICAL CENT.

(UVI-) UNIV VIRGINIA PATENT FOUND.

PI Conincili F, Pizarro T, Rotter JI, Yang H;

Conincili F, Pizarro T, Rotter JI, Yang H;

WFI: 97-372880/34.

PT Actecting allele 2 of the VNTR (variable number of tandem repeats)

PT Actecting allele 2 of the VNTR (variable number of tandem repeats)

PT POLYMORPHISM at intron 2 of the IL-1 receptor antagonist gene

Claim 7; Page 17; 22pp; English.

CC This PCR primer and primer T89948 are used to amplify intron 2 of the Unman interleukin-1 receptor antagonist gene (IL-1ra) in a novel method con consecutive colitis (UC) in a subject of Jewish ancestry.

CC There is an association between allele 2 of the variable number of tandem crepeats (VNTR) polymorphism at intron 2 of IL-1ra, an important conceptry. This method can be used for the diagnosis and prognosis of UC in Jewish patients for UC and distinguishing UC in humans of Jewish can other inflammatory disease of the bowel.

Sequence 17 BP; 5 A; 7 C; 1 G; 4 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                        05-WAR-1998 (first entry)
Muman Interleukin-1 receptor antagonist intron 2 PCR primer 1.
Interleukin-1 receptor antagonist; IL-1ra; ulcerative colitis;
diagnosis; prognosis; inflammatory bowel disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-ARR-1998 (first entry)
Human IL-1RN gene intron 2 PCR primer 1.
Osteoporosis; interleukin-1 receptor antagonist; IL-1RN; allele;
bone mineral density; post-menopause; PCR primer; ss.
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W09738135-Al.

16-OCT-1997.

03-APR-1997; U05626.

05-APR-1996; US-628282.

(MEDI-) MEDICAL SCI SYSTEMS INC.

DDIF GW. Eastell R, Russell G;

WPI; 97-512741/47.
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                                     standard; DNA; 17 BP.
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T89409;
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Best Local Similarity 100.
Matches 17; Conservative
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Homo sapiens.
WO9725445-A1.
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                                     T89947
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RESULT
T89947
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25-NOV-1998 (first entry)
PCR primer used to amplify interleukin-1 receptor antagonist (IL-1RN).
Interleukin-1 receptor antagonist; IL-1RN; predisposition;
coronary artery disease; screen; PCR primer; ss.

V60230 standard; DNA; 17 BP.

RESULT V60230 Detection of predisposition to coronary artery disease - by comparative measurement of levels of expression of alleles from the

17-SEP-1998.
09-MAR-1998; U04725.
10-MAR-1997; US-813456.
(MEDI-) MEDICAL SCI SYSTEMS INC.
CROSSMAN DC, DULÍ GW, FrANCIS SE;
WPI; 98-520829/44.

WO9840517-A1.

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Jampucins occur.

Interleukin-IRN (IL-IRN) primers 1 and 2 (V32394) were used to amplify the IL-IRN permers 1 and 2 (V32394) were used to amplify the IL-IRN mentered and identify polymorphism of the VWTR region to the IL-IRN and recome a signal threatening diabetic retinopathy. The method involves isolating DNA from a patient and determining the DNA polymorphism pattern of the genes that code for interleukin-I-alpha, interleukin-I-beta and interleukin-IRN. The polymorphic pattern identified is then compared with controls of known DNA polymorphism associated with increased with controls of known DNA polymorphism associated with increased risk of sight threatening diabetic retinopathy. The method may be able to identify diabetic patients at risk before the clinically detectable disorders occur. Polymorphism pattern determination of IL genes involved PCR reactions using primers vizable disorders occur. Polymorphism pattern determination of other genes associated with sight threatening diabetic retinopathy in genomic DNA and therefore, in identifying sentence 17 BP; 5 A; 7 C; 1 G; 4 T;
                                                                                                                                                                                                                                                                                                             ö
a variable number tandem repeat (VNTR) region that gives rise to five allelles. This product is used for predicting the risk of osteoporosis in a subject by determining the allellic and genetic polymorphism pattern for IL-1RN in genomic DNA. A pattern of at least one copy of the IL-1RN allele 2 indicates an increased susceptibility to osteoporosis. The methods can predict low bone mineral density (BMD) and the rate of bone density loss and thereby a susceptibility to osteoporosis. Individuals so identified can then be treated more aggressively to prevent or retard the occurrence of disease.
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-1RN primer 1. Genetic publication; interleukin-1RN; Genetic polymorphism; PCR; primer; amplification; interleukin-1RN; sight threatening diabetic retinopathy; interleukin-1-alpha; IL-1RN; interleukin-1-beta; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Predicting increased risk of sight-threatening diabetic retinopathy comprises identifying genetic polymorphism pattern for genes IL-1A, IL-1B and IL-1RN, useful to allow treatment before clinical
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                               DB 1; Length 17;
                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                   4 T;
                                                                                                                                                                                                                                                                                     Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                 1 G;
                                                                                                                                                                                                                                                               100.0%; Score 17; 100.0%; Pred No. 1
                                                                                                                                                                                                 7
C;
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09-OCT-1997; G02790.
10-OCT-1996; GB-021129.
(DUFF,) DUFF G.
(RENN/) RENNIE I.
(RICH/) RICHARDSON R.
DUÍF G. RENNIE I, RICHARDSON R.
WPI: 98-240835/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V32393 standard; DNA; 17 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-SEP-1998 (first entry)
                                                                                                                                                                                                 5 A;
                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.
Matches 17: Conservative
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WO9815653-A1.
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A method has been developed for the diagnosis of osteoporosis comprising determining the genotype of an interleukin-1 (IL-1) receptor antagonist gene (IL-IRN). The present sequence represents a PCR primer adapted to amplify a portion of intron 2 of an IL-IRN for use in the method of the invention. The method can be used for the diagnosis of disease, including diagnosis of osteoporosis and predisposition or susceptibility
                                                                                                                                                                                                                                             interleukin 1 docus Claim 6: Page 15: 22pp; English.

Claim 6: Page 15: 22pp; English.

Claim 6: Page 15: 22pp; English.

the interleukin-1 receptor antagonist (IL-1RN). The specification describes a method for determination of a patient's predisposition to coronary artery disease. The method comprises comparing an allele with a second allele which is predistive of coronary artery disease, where similarity between the first and second alleles indicates a predisposition to coronary artery disease. The method is used to genotype an individual's interleukin (IL)-1 loci, the overexpression of which correlates with coronary artery disease. The method is used to screen a patients' predisposition to coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IL-1 receptor antagonist gene intron 2 PCR primer #1.
Human; interleukin-1 receptor antagonist gene; IL-1; polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosis of osteoporosis by determining genotype of interleukin-l receptor antagonist gene - useful for diagnosing patient pre-disposition or susceptibility to osteoporosis and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis; osteoporosis; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 A;
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les 17; Conservative
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27-MAR-1998; G00944.
27-MAR-1997; GR-006359.
(GEMI-) GEMINI RES LTD.
Keen RW, Spect v TD;
WPI; 98-557135/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     artery disease.
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WO9844150-A1.
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Best Local S:
Matches 17,
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Gaps

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Mismatches

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1 CTCAGCAACACTCCTAT 17 1 CTCAGCAACACTCCTAT 17 17; Conservative

100.0%; Score 17; DB 1; Length 17; 100.0%; Pred. No. 1.3;

Query Match Best Local Similarity

Matches

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Conservative
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09-DEC-1996; G03043.
11-OCT-1996; GB-021295.
07-DEC-1996; GB-026004.
23-MAY-1996; GB-010824.
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Best Local Similarity
Matches 17; Conserv
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WO9720932-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, page 21-27; 36pp; English.

A method has been developed for the disgnosis of osteoporosis comprising determining the genotype of an interleukin-1 (IL-1) receptor antagonist gene (IL-IRN). The present sequence represents the human interleukin-1 receptor antagonist gene. The method can be used for the diagnosis of disease, including diagnosis of osteoporosis and predisposition or susceptibility to osteoporosis and for therapy.

Sequence 12565 BP; 3217 A; 2980 C; 3072 G; 3294 T;
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Interleukin 1 (44112332) haplotype PCR primer #15.
Interleukin 1: IL-1; haplotype; inflammatory disorder; alopecia areata; coronary artery disease; osteoporosis; nephropathy; diabetes mellitus; Graves disease; systemic lupus erythamatosus; lichen sclerosis;
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                           Diagnosis of osteoporosis by determining genotype of interleukin-l receptor antagonist gene - useful for diagnosing patient pre-disposition or susceptibility to esteoporosis and for
                                                                                                                                                                                                         19-JāN-1999 (first entry)
Human interleukin-1 receptor antagonist gene.
Human: interleukin-1 receptor antagonist gene; IL-1; polymorphism;
diagnosis; osteoporosis; ds.
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                                                Score 17; DB 1; Length 17;
Pred. No. 1.3;
Mismatches 0; Indels
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DE GIOVINE F S.

DUFF G.

COX A, De Giovine FS, Duff G;
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 to osteoporosis and for therapy Sequence 17 BP; 5 A; 7
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                                                                                                                                                                                   V62392 standard; DNA; 12565 BP.
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                                                                        17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                therapeutic intervention
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27-MAR-1998; G00944.
27-MAR-1997; GB-006359.
(GEMI-) GEMINI RES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-1998; G01481.
29-MAY-1997; GB-011040.
(CAMP/) CAMP N J.
                                                                                                                                                                                                                                                                                                                                      Spector ID;
                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                            Homo sapiens.
WO9844150-A1.
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WO9854359-A1.
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                                                Query Match
                                                                                                                                                                                                                                                                                                                                     Keen RW,
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(DGIO/)
                                                              Local
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                                                             Best Loca
Matches
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V62392
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WPI: 99-080814/07.

PT Wew method of determining a patient's susceptibility to inflammatory proveduced by detecting the presence of an IL-1 (44112312)

Talsolotype, useful in designing treatment strategies that modulate produced by the IL-1 (44112312)

PT Claim 31: Apge 31: 49pp: English

C Claim 31: Apge 31: 49pp: English

C C an inflammatory disorder. The method comprises the detection of an inflammatory disorder. The method comprises the detection of an inflammatory disorder. The method comprises the method from the carlent, where its presence indicates susceptibility to an inflammatory disorder. The method comprises in the method for detecting the IL-1 (44112312) haplotype in a sample obtained from the carlent, where its presence indicates susceptibility to an inflammatory disorder. X16607 to X16631 represent PCF primer used in the method for detecting the IL-1 (44112312) haplotype. The method provides kits for disorders, including coronary artery disease, osteoporosis, nephropathy in disorders, including coronary artery disease, osteoporosis, nephropathy coronary artery disease, osteoporosis, nephropathy corpused and alletes of the haplotype can be applied to particular inflammatory coronary artery disease. Systemic lupus alletes of the haplotype enables determination of which alletes are disorders, including diabetic retinopathy, juvenile chronic arthritis, producinate the activity of proteins produced by the IL-1 gene cluster of that modulate the activity of proteins produced by the IL-1 gene cluster of inflammatory diseases, and insufficient IL-1 production appears to act contrally in the pathology of these diseases. Therefore, the use of IL-1 gene clusters is useful in determining genetic susceptibility to gene clusters is useful in determining genetic susceptibility to with a molygenic commonent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 1a; 128pp; English.
This nucleotide sequence codes for the heavy chain variable region (WH) (WH)881) of human carcinoembryonic antigen (hCEA)-specific antibody CEA6. WH (T72126-32) and VL (T72133-35) gene sequences were determined for anti-hCEA antibodies CEA1-CEA7 (see W19876-85) that had been obtained by selection from a universal phage display library. A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Carcinoembryonic antigen; CEA; human; antibody; scFv;
tumour marker; lung cancer; breast cancer; colon cancer;
adenocarcinoma; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CAMB.) CAMBRIDGE ANTIBODY TECHNOLOGY
Allen DJ, McCafferty JG, Osbourn JK
WPI; 97-319779/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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CEA-specific antibody CEA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTCAGCACACTCCTAT 17
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Example 4; Page 63-64; 110pp; English.

Example 4: Page 63-64; 110pp; English.

The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural construct comprise at least one tetranectin trimerising structural construct comprise at least one tetranectin trimerising structural construct (TYES) which is covalently linked to at least one heterologous moiety, the TYES being capable of forming a stable complex with 2 other TYES, with the proviso that the heterologous moiety is different from carry of the fusion proteins clinkernv12, Merryn12, Merryn12, Herryn13, GW4261, THE TYES can be used for the construction of conjugates with heterologous moieties such as a ligand binding structure, a redioactive moiety, a cytokine, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, an non-proteinaceous polymer, a photo construct to a tranget. They can be used as vehicles for a radioactive moiety fragments into oligomeric or multivalent entities for generating chimeric artificial antibodies having preselected pharmacoxinetic and/or pharmacynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of tissue or for delivering an imaging or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a disease or the formatic or a release of the material for a wide variety of conjugates. The cans are as a conformative for a wide variety of conjugates. The restrict of a release of confugates. The restrict of a prevention of trimeries of confugates a stable structure which can act as a conformative which energy and the construction of trimeries of a nucleotide sequence encoding a Cabá antibody single-chair (sock) fragment. This is used in the construction of t
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEA6 antibody single-chain Fv (scFv) fragment encoding DNA.

Trimcric polypeptide; tetranectin trimcrising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; CEA6; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; ss.
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                  with human liver cells, and preferentially binds to the A3-B2 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA-T, or their CEA sequences, as well as CEAE, VH and VL variants. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer sequence 369 BP; 85 A; 101 C; 109 G; 74 T;
     is non-cross-reactive
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                                                                                                                                                                                                                                                                                      Score 14.4; DB 1; Length 369; Pred. No. 45;
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  constant for hCEA of less than 1 x 10 -8 M,
                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Larsen IK, Nielsen BB, Thogersen HC;
WPI; 99-080897/07.
                                                                                                                                                                                                                                                                                      84.78;
93.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X05452 standard; DNA; 786 BP.
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                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  86 TCAGCAACTCTCCTAT 101
                                                                                                                                                                                                                                                                                                                                                                                       2 TCAGCAACACTCCTAT 17
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11-JUN-1998; DK0245.
11-JUN-1997; DK-000685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GRAV/) GRAVERSEN N J H. (HOLT/) HOLTET T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KAST/) KASTRUP J S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ETZE/) ETZERODT M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9856906-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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The products for diagnosis, prevention and treatment of hypoglycaemia, products for diagnosis, prevention and treatment of hypoglycaemia, diabetes, neuronal disorders and tumours.

The diabetes, neuronal disorders and tumours.

A method has been developed for testing the developmental status in particular form of the mammal; and/or (b) determining the parcreatic cells (PGS) of a mammal; and/or (b) determining the cor status of Pax6 mRNA in PCs of the mammal; and/or (c) comparing or status of Pax6 mRNA and/or Pax6 protein with the corresponding level in normal PCs. The present sequence encodes pax6 protein. The method can be used for determining the developmental status of PCs as indicative of hypoglycaemia, diabetes, neuronal disorders or temporates. The products can be used for developing agents for treating or reventing such disorders.

Sequence 2481 BP; 743 A; 554 C; 571 G; 613 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; Pax4; Pax6; pancreatic cell; differentiation status; tumour; developmental status; transgenic mammal; diabetes; neuronal disorder; ss.
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                  Mouse; Pax6; Pax4; pancreatic cell; differentiation status; developmental status; transgenic mammal; hypoglycaemia; diabetes;
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0
                                                            Length 786;
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                                                                                            Indels
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                    161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN. Gruss P. St-Onge L; WPI; 98-388143/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.4%; Score 14; DB 1; 100.0%; Pred. No. 92;
                  227
                                                              DB
                                                                                          Mismatches
                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                            Score 14.4;
Pred. No. 49
                  ΰ
                  211
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                              /product= "Pax6"
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                                                                                                                                                                                                                               BP
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                                                                                                                                                                                                                                                                                                                    neuronal disorder; tumour; ss.
                  Ä
                                                           84.7%;
93.8%;
                                                                                                                                                                                                                          V40019 standard; cDNA; 2481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-1998 (first entry)
Mouse Pax6 gene SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                163. .1473
/*tag= a
                 187
                                                                                                                                                                                                                                                      12-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163. .1473
/*tag= a
                                                                                                                                      86 TCAGCAACTCTCCTAT 101
                                                                                          Conservative
                                                                                                                     2 TCAGCAACACTCCTAT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CAGCAACACTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1997; E07320
                                                         Query Match
Best Local Similarity
Matches 15; Conserv
 scFv antibodies.
Sequence 786 BP;
                                                                                                                                                                                                                                                                       Mouse Pax6 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; W69509
                                                                                                                                                                                                                                                                                                                                                                                                            WO9829565-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUL-1998.
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                                                                                                                                                                                                                                           V40019;
                                                                                                                                                                                                                                                                                                                                    Mus sp.
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ID V4
AC V4
AC V4
DJ I2
DE MC
KW MC
KW GE
CS MU
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V81414
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Products for diagnosis, prevention and treatment of diabetes,

products for diagnosis, prevention and treatment of diabetes,

neuronal disorders and tumours

Clavel and the correct and tumours

Clavel or status of Paralish.

A method has been developed for testing the developmental status in parcreatic cells (PC's) of a mammal comprising: (a) determining the level or status of Paral protein in PC's of the mammal; and/or (b)

Clavel or status of Paral mixed and the mammal; and/or (b)

determining the level or status of Paral mixed in PC's of the mammal;

and (c) comparing the level or status of Paral mixed in PC's of the mammal;

clavel or responding level in normal PC's. The present invention also describes a nucleic acid sequence encoding a functional and expressible Para protein, for the preparation of a therespectic composition for treating, preventing and/or delaying diabetes and/or a neuronal disorder in a mammal. The present sequence encodes a Para protein. The method can be used for determining the temoris. The products can be used for developing agents for treating the those diabetes.
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This full-length cDNA clone, designated do568 11, codes for a novel secreted human protein (see W79094). It was isolated from a human adult testis cDNA library using methods which are selective for CDNAs encoding secreted proteins, or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the encoding protein. The nucleotide sequence shows homology to some database sequences. The invention provides cDNA clones (see V61477-87) from human foetal kidney, adult testis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-1998.
19-MAR-1998; U05474.
18-MAR-1998; U05474.
19-MAR-1999; UG-240063.
19-MAR-1997: UG-820493.
(GEMY ) GENETICS INST INC.
Agostino MJ, Jacobs K, LaVallie ER, McCoy JM, Merberg D,
Agostino MJ, Jacobs K, LaVallie ER, McCoy JM, Merberg D,
WPI: 98-521163/44.
P-PSDB: W79094.
New polynucleotide(s) encoding secreted human proteins - derived from human foetal kidney, adult testes and adult or foetal brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.4%; Score 14; DB 1; Length 2481; 100.0%; Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 571 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 92;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 554 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JAN-1999 (first entry)

Human secreted protein do568_11 cDNA.
Secreted protein; human; do568_11; ds.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.4°,
100.0%; Pre
0; '
/product= "Pax6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V61485/C
ID V61485 standard; cDNA; 2245 BP.
A.C V61485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               743 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359. .1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.4
Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038 CAGCAACACTCCTA 1051
                                                                   31-DEC-1996; US-778423.
                                                                                                    Gruss P, Sosa-Pineda B;
WPI; 98-388144/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CAGCAACACTCCTA 16
                                               30-DEC-1997; E07321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2481 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               these disorders.
                                                                                                                                     P-PSDB; W69513
              W09829566-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9841539-A2.
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Tproliferative diseases

Claim 12; Page 67-70; 95pp; English.

This CDNA clone codes for a new human prenylcysteine carboxyl

This CDNA clone codes for a new human prenylcysteine carboxyl

C methyltransferase (PCCMT, see W67730) involved in post-translational

C modification of prenylated proteins. It was isolated following

an EST database search for mammalian sequences related to the

C saccharomyces cerevisiae isoprenylcysteine methyltransferase Steld

G see PR primers (see W1415-16) based on an isolated EST were

CC used in a PCR amplification of human HL60 cell cDNA. A PCR product

CC (see V81417) was used to screen an HL60 cell cDNA. A PCR product

CC (see V81417) was used to screen an HL60 coll incary to isolate

CC steld was 26%. Also new are an expression vector containing DNA

CC steld was 26%. Also new are an expression vector containing DNA

CC cncoding human PCCMT. hosts transformed with this vector, compounds

CC for PCCMR: and a method for screening for, and isolating,

CC inhibitors of PCCMT. The inhibitors are used to treat inflammation,

CC cancer and other hyperproliferative diseases such as psoriasis, e.g.

CC by inhibiting prenylation of Ras proteins. PCCMT is also used as a
and adult or foetal brain cDNA libraries that code for secreted proteins (see W79087-97). These clones are deposited as ATCC 98364. The polynucleotides and proteins are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional, immune stimulating (e.g. as cativities include nutritional, immune stimulating (e.g. as cativitylinhibin, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, antiinflammatory, cadherin/tumour invasion suppressor and tumour inhibition activities. The polynucleotides are also stated to be useful for gene therapy. Sequence 2245 BP; 443 A; 632 C; 617 G; 546 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by inhibiting prenylation of Ras proteins. PCCMT is also used as a reagent for carboxy methylation of substrates, e.g. to produce functional Ras proteins, and for raising Ab. When over-expressed in a cell, peptide fragments of PCCMT may act as inhibitors. Fragments of PCCMT mucheic acids are used as probes to isolate related sequences from other sources, and nucleic acids expressing a dominant negative variant of PCCMT can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mammalian prenylcysteine carboxyl methyltransferase - and its
inhibitors, useful for treating inflammation, cancer and other
proliferative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-ARR-1999 (first entry)
Human prenylcysteine carboxyl methyltransferase cDNA.
Prenylcysteine carboxyl methyltransferase; PCCMT; human;
inhibitor; screening; inflammation; cancer; cell proliferation;
psoriasis; Ras protein; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14; DB 1; Length 2245; Pred. No. 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.4%; Scor.
v 100.0%; Pred. No. >1.
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.(
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44. .898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 99-070326/06.
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968 T;

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Matches
                                                                                                                                                                                                                              X37439/c
                                                                                                                                                                                                                                                                                        resolution and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders claim la; Page 196: 280pp; English or blood disorders claim la; Page 196: 280pp; English or blood disorders claim la; Page 196: 280pp; English or blood disorders and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions are useful for preventing, the presence or amount of expression of diagnosed by determining the presence or amount of expression of the new polypeptides in a sample or by determining the presence or amount of expression of the new polypeptides. Specific uses are absence of mutations in the new polynuclectides. Specific uses are absence of mutations in the new polynuclectides. Specific uses are absence of mutations in the new polynuclectides. Specific uses are absence of mutations in the new polynuclectides. Specific uses are described for each of the 70 polynuclectides. Specific uses are disorders, developmental abnormalities and focetal deficiencies, blood disorders, leukenias, diseases of the immune system, autoimmune diseases, hepsitic and renal diseases of the immune system, autoimmune diseases, hepsitic and renal diseases. lymphomas, inflammation, allergies, asthma, sepsis, diabetes, Alzhritis, psoriasis, digestive/endocrine disorders, of the invention are content and AIDS. The human secreted proteins of the invention are content and and all and an are content and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein cDMA fragment containing gene 11.

Human: secreted protein; prevention; treatment; protein therapy;

Human; secreted protein; prevention; treatment; protein therapy;

developmental adiagnosis; cancer; tumour; neurodegenerative disorder;

leukemia; immune system disorder; autoimmune disease; hepatic disease;

renal disease; inflammation; allergy; asthma; sepsis, diabetes, AIDS;

Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis;

arthritis; psoriasis; digestive; endocrine; infection; ss.
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represented in Y07744-Y07850 and the encoding nucleic acids are
                                                                                                          ;
0
                                                DB 1; Length 3597; 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
Brewer LA, Duan R, Ebner R, Endress GA, Feng P,
Florence CA, Florence RA, Komatsoulis GA, Lafleur DW,
Moore PA, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR,
                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584 G;
                                                                               Pred. No. 96;
Mismatches
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                                                   Score 14;
                                                      82.4°,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                          X37379 standard; cDNA; 2084 BP.
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                                                   82.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1999 (first entry)
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18-AuG-1998; US-092956.

15-UU-1998; US-092956.

19-AuG-1997; US-056368.

19-AuG-1997; US-056368.

19-AuG-1997; US-056369.

19-AuG-1997; US-056555.

19-AuG-1997; US-056528.

19-AuG-1997; US-056528.

19-AuG-1997; US-056629.

19-AuG-1997; US-056726.
                                                                                                             14; Conservative
                                                                                                                                                                                                                              1263 CTCAGCAACACTCC 1276
                                                                                                                                                                    1 CTCAGCAACACTCC 14
                                                                                  Best Local Similarity
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WO9909155-A1.
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                                                      Query Match
                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                RESULT 1

X37379/C

X37379/C

X37379/C

X37379/C

X37379/C

X37379/C

X37379/C

X37379/C

X8W Buma

RWW Buma

RWW AICHA

RWW I19-A

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DB 1; Length 2084; 90;

Score 14; Pred. No.

82.4%; 100.0%;

Query Match Best Local Similarity

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New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disolateds, immune diseases, inflammation or blood disorders claim la: Page 230; 280pp; English.

This invention describes novel isolated human secreted proteins and their encoding nucleic acid sequences. The products of the invention are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions e.g. by protein or gene therapy. Also pathological conditions can be the new polypeptides in a sample or by determining the presence or amount of expression of the new polypeptides in the new polynucleotides. Specific uses are described for each of the 70 polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative diagnosis or treatment of cancer, tumours, neurodegenerative diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein conversions treatment; protein therapy; Human; secreted protein prevention; treatment; protein therapy; agene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; foetal deficiency; blood disorder; lymphoma; leukemia; immune system disorder; autoimmune disease; hepatic disease; renal disease; inflammation; allergy; asthma; sepais; diabetes; AIDS; Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis; arthritis; psoriasis; digestive; endocrine; infection; ss.
Gaps
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19-AUG-1997; US-056535.

19-AUG-1997; US-056528.

19-AUG-1997; US-056628.

19-AUG-1997; US-056629.

19-AUG-1997; US-056728.

10-AUG-1997; US-056728
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100.0%; Pred. No. 90;
'... 0; Mismatches
     Mismatches
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Best Local Similarity 100.
Matches 14; Conservative
14; Conservative
                                                                                                                                                1235 CAGCAACACTCCTA 1222
                                                                                            3 CAGCAACACTCCTA 16
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P-PSDB; X07814
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19-AUG-1997; U
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19-AUG-1997;
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Search completed: September 18, 1999, 05:27:21 Job time: 1686 sec

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DEFINITION
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NID
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T71181
LOCUS
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                                                   7 ; Search time 1405 Seconds
(without alignments)
23.867 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                        986266752 residues
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                                  nucleic search, using sw model
                                                                                   US-09-037-472-5
17
1 CTCAGCAACACTCCTAT 17
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Perfect score:
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                                  nucleic
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AA102335 2199505.5
AA122310 22806.5
AA135360 2025603.5
AA35914 C28914 Rice
A28914 C28914 Rice
A1290208 4179910.x
D34140 CELK041E9R
W75479 W576212.r1
AA39139 LD10274.5
AK038231 AR0538251
AA039230 LD10274.5
AI037320 LE00306.5
AI258185 LR001318.5
AI353647 Zeb0805.5
AI477924 f649505.x
AI477320 f635901.x
AI37320 f635901.x
AI37320 f635901.x
AI37320 f635901.x
AA17329 y9777f10.r1
H47705 y977f10.r1
                                                                                                                                                                                                                                                                                                     D34472 CELK046D4R
D34568 CELK008G8R
D35963 CELK027E5F
M78523 EST00671 Fe
T24016 seg2172 3HF
T67556 yd12h07.s1
A1046863 Homo sapi
                                                                                    T71181 yc52d04.rl
                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                          Description
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                                                        SUMMARIES
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T24016
T67556
HSM011713
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AA135360
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C28914
AI290208
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AI040382
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AA415740
AA933081
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HSM006824
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AI402823
AI467191
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55:
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393 bp mRNA EST 01-MAR-1995 ycc2dd4.rl Stratagene liver (#937224) Homo sapiens cDNA clone T71181 g685702 T71181.1 G1:685702

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS TITLE JOURNAL MEDLINE COMMENT

```
1 (bases I to 540)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 433)
Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rikkin, L.,
Trevaskis, E., Underwood, K., Soares, M.B., Tan, F., Thierry-Meg, J.,
and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2188a06.s1 Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:511666 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                       Fmail: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 441.
Location/Qualifiers
1. .540
/organism="Homo sapiens"
/db_xref="GDB:3844448"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                     REFERENCE
                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High qality sequence stops: 306 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 736 Std Error: 0.00
                                                                                             (bases 1 to 393)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Hillier, D., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA102335 540 bp mRNA EST 31-JUL-1997 z191b05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511953 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                       Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                     On Sep 21, 1992 this sequence version replaced gi:276333
                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:84295"
/clone_lib="Stratagene liver (#937224)"
/sex="male"
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/db_xref="GDB:501352"
/db_xref="taxon:9606"
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Location/Qualifiers
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Best Local Similarity 100.
Matches 17; Conservative
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AA102335.1
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              human.
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FEATURES

LOCUS

ACCESSION

ORGANISM

KEYWORDS SOURCE

VERSION

RESULT 2 AA102335/c

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BASE COUNT ORIGIN

Gaps

TITLE JOURNAL MEDLINE COMMENT

FEATURES

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M.D., ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: N.L.GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA587215 495 bp mRNA EST 26-SEP-1997 nn82a06.s1 NCI_CGAP_CO9 Homo sapiens cDNA clone IMAGE:1090354 3' Samilar to contains Alu repetitive element;, mRNA sequence. 92398029 434587215.1 GI:2398029
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           Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consorium (info@image.llnl.gov) for further information. Insert Length: 2139 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 81.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Unpublished (1997)
On Sep 1, 1995 this sequence version replaced
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100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0;
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Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 477.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 100.
Matches 15; Conservative
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AA587215/c
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TITLE
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Trevsskis, E., Underwood, K., Soares, M.B., Tan, F., Thierry-Meg, J., and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA135360 483 bp mRNA EST 06-AUG-1997 2025e03.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587932 3' similar to contains Alu repetitive element;, mRNA
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97044478
Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 371.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                             On May 18, 1995 this sequence version replaced gi:811366
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                  63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 433;
                                                                                                               Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 1
11 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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1.6e+02;
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:3844161"
/db_xref="taxon:9606"
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AA135360.1 GI:1696464
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Best Local Similarity 100.
Matches 15; Conservative
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AA135360/c LOCUS DEFINITION

RESULT

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ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL MEDLINE COMMENT

BASE COUNT ORIGIN

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93931862
AI290208.1 GI:3931862
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Best Local Similarity 100.
Matches 15; Conservative
                93 CAGCAACACTCCTAT 107
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3 CAGCAACACT: CTAT 17
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KEYWORDS
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                                                  The following the colon, vector: pT7T3D-pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from REH colon tumor, and was then primed with a Not I coligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 constructed by Bento Soares and M. Fatima Bonaldo (Soares4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           C28914 385 bp mRNA EST 06-AUG-1997 C28914 Rice callus cDNA Oryza sativa cDNA clone C62810_1A, mRNA
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                                                                                                                                                                                                                                                  Score 15; DB 35; Length 43:
Pred. No. 1.6e+02;
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Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
     /clone_lib="NCI_CGAP_Co9"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Rice callus cDNA"
/tissue_type="callus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tsasaki@abr.affrc.go.jp.
Location/Qualifiers
                                                                                                                                                                                                   122 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="callus"
85 c 78 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="4"
/clone="C62810_1A"
                                                                                                                                                                                                                                                     88.2%; Scur
100.0%; Pre
0; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 385)
Yamamoto, K. and Sasaki, T.
Rice cDNA from callus 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g2312759
C28914.1 GI:2312759
                                                                                                                                                                                                    128 c
                                                                                                                                                                                                                                                               Query Match 88.2
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                   403 CTCAGCAACACTCCT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 15: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poaceae; Oryza.
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C28914
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AUTHORS
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RESULT 7

A120008C

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ORGANISM

SOURCE

VERSION KEYWORDS

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 563)
Martam M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W75479 563 bp mRNA EST 20-JUN-1996 me56a02.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:391466 5' similar to gb:M64241 QM PROTEIN (HUMAN); gb:M93980 Mouse 24.6 kda protein mRNA, complete cds (MOUSE);, mRNA
      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1316 Std Brror: 0.00
Seq primer: T7
High quality sequence stop: 1.
Location/Qualifiers
1. 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
WashU-HMIM Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
MGI:243298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:692592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.4; DB 25; Length 235;
Pred. No. 3e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:3796108"
/db_xref="taxon:9606"
/clone="IMAGE:246862"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
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93.88;
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W75479.1 GI:1385758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                    source
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ORIGIN
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AUTHORS
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W75479/c
LOCUS
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                                    Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 366)
Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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yv57e12.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Prinates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 235)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Markins,M., Hultman,M., Kucaba,T., Lecy,M., Le,N., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Travaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Milson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_1bb="Yk1eg"
/clone_lib="Yuji Kohara unpublished cDNA"
/note="dev_stage=varied, sex=Hermaphrodite male, tissue_type=whole animal"
48 c 92 q 89 t 2 others
                                                                                                                                                                                                               Unpublished (1994)
On Sep 21, 1992 this sequence version replaced gi:276221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Apr 14, 1993 this sequence version replaced gi:635823
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 366;
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                                                                                                                                                                                               C.elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                 Gene Library Lab
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Tel: 0559-75-0771
Fax: 0559-75-6240
Email: ykohara@ddbj.nig.ac.j.
Location/Qualifiers
ce 1. 366
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Pred. No. 3.3e+02;
0; Mismatches 2;
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                                                                                                                                                                                      Toward an expression map of the Unpublished (1994)
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88.2%;
                                                                                                                                                                                                                                                                             Contact: Yuji Kohara
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N58629.1 GI:1202519
GI:525049
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Matches 15; Conserv
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D34140.1
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Query Match

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BASE COUNT ORIGIN

SOURCE

KEYWORDS

VERSION

REFERENCE AUTHORS TITLE JOURNAL MEDLINE COMMENT

LOCUS

N58629/c

RESULT

ACCESSION

source

FEATURES

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Gaps

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Gaps

0;

FEATURES

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/clone_liber.to Drosophila melanogaster embryo BlueScript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/dab_host="Solm"
/note="Organ: embryo; Vector: BlueScript SK; Site_1:
BooR: Site_2: Xhol; Constructed using Stratagene ZAP-cDNA
Synthesis kit. Oligo dT-primed and directionally cloned at
EcoRI and Xhol in BlueScript SK(+/-)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A1040382 438 bp mRNA EST 28-AUG-1998 ox16c10.x1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF038251 2374 bp mRNA EST 30-MAR-1998 AF038251 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntBlcon, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2374)
Tripodis, N. and Ragoussis, J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 boundary
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2045088.
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                                                                                                                                                                                                                                                          Length 629;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guys Hospital
7th floor, Guy's Tower, London SEl 9RT, UK
Email: nikos@nki.nl.
Location/Qualifiers
                                                                                                                                                                                                                                                        84.7%; Score 14.4; DB 38;
93.8%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14.4; DB 39;
Pred. No. 4.7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="6p21.3"
/clone="ntBlcon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Human mRNA
584 c 628 g 6
                           /clone="LD10274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92815881
AF038251.1 GI:2815881
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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Les 15, Conservative
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AIO40382/C
LOCUS
DEFINITION
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AF038251
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LD10274.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD10274 5prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 629)
Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
Brokstein,P., Lewis,S. and Rubin,G.M.

BOGP/HHMI Drosophila EST Project
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On Jan 17, 1998 this sequence version replaced gi:2044375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                        /clone_lib="Soares mouse embryo NbME13.5 14.5" /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                              /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/db_xref="BDGP_EST:BDcln009541"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.4; DB 26;
Pred. No. 3.6e+02;
0; Mismatches 1;
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G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
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                                                        1. .563
/organism="Mus musculus"
Seg primer: ETPrimer
High quality sequence stop: 325.
Location/Qualifiers
                                                                                                          /db_xref="taxon:10090"
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                                                                                          /strain="C57BL/6J"
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AA391390.1 GI:2790692
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93.8%;
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AA391390/c
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KEYWORDS

VERSION

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FEATURES

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Gaps

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/organism="Drosophila melanogaster'
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/clone="LP06306"
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93.8%;
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                                                                                                        Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Bukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 438)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                    Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (life@image.llnl.gov) for further information. Insert Length: 983 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 383.
Location/Qualifiers
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 551)
Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,
                                                                                                                                                                                                                      Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:2043603
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/sex="male"
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Pred. No. 3.4e+02;
0; Mismatches 1; Indels 0;
clone IMAGE:1656498 3', mRNA sequence.
A1040382
                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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AI257823.1 GI:3865348
                                                      Ā1040382.1 GI:3279576
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93.88;
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Best Local Similarity 93.8
Matches 15; Conservative
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/clone_lib="LP Drosophila melanogaster larval-early pupal
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                                                                                                                                                                                                                                                                                                                                                                        G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 63 row: A column: 6
High quality sequence stop: 548.
Location/Qualifiers
1. 551
/organism="brosophila melanogaster"
/db_xref="taxon:7227"
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Drosophila melanogaster

Drosophila melanogaster

Bikaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 633)

Harvey, D., Hongi,L., Evans-Holm,M., Pendleton,J., Su,C.,

Brokstein,P., Lewis,S. and Rubin,G.M.

BDGP/HHMI Drosophila EST Project

Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2151868.
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G. M. Rubin Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Fax: 510 sequence Sequen
Brokstein,P., Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2151047.
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Pred. No. 3.5e+02;
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/lab_host="DH5-alpha"
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pOT2"
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/lab_host="DH5-alpha"
/note="Organ: whole body; Vector: pOT2; Site_1: EcoRI;
Site_2: Xhol; Sized fractionated cDNAs were directly
ligated into pOT2. Plasmid cDNA library.
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168 g 119 t 151 c 195 a BASE COUNT ORIGIN

ö Gaps Query Match

84.7%; Score 14.4; DB 44; Length 633;

Best Local Similarity 93.8%; Pred. No. 3.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0;

QQ ò

Search completed: September 18, 1999, 06:47:40 Job time: 3657 sec

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September 18, 1999, 15:48:49; Search time 436.05 Seconds (without alignments) 145.869 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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1: 9b_bal:*

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10: 9b_pr:*

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16: 9b_or:*

17: 9b_vi:*

18: em_hum:*

19: em_hum:*

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I73228 Sequence 4

20 5 173228

20 100.0

Description

X04500 Human gene AF026543 Bos tauru AF004147 Homo sapi 278059 Caenorhabdi AC007535 Homo sapi AC003029 Homo sapi AC007316 Homo sapi U38377 Caenorhabdi AC00736 Homo sapi U65668 Lycopersico U81378 Lycopersico	AC000380 Home sapi AL04958 Home sapi AC007624 Home sapi AC007540 Home sapi AC0071249 Danio rer Y07696 D. rerio Hox 122487 Sequence 23 U19382 Arabidopsis AL03134 S. pombe c AL03134 S. pombe c AL03134 B. pombe c AL03134 B. pombe c AL03134 B. man DNA s AL03134 B. man DNA s AL02144 Human DNA s AL02166 Human DNA AL02166 Human DNA AL02166 Human DNA AL031666 Human DNA AL031666 Human DNSP AL03171 Human Phosp AL031736 Human DNA AC004617 Home sapien AC004617 Home sapien AC006210 Home sapien AC006210 Home sapien AC006210 Home sapien AC006211 Home sapien AC006211 Home sapien AC00632 Muman Deta4 U52111 Home sapien AC006604 Home sapien AC006604 Home sapien AC006608 Caenerhab	PAT 23-DEC-1997 periodontal disease
HSILIB AF026543 AC004147 AC004147 AC007535 AC007316 CELK08A8 AC007316 LEU65668 LEU65668 LEU65668	HSAC000380 HSJ169P2 AC00752 AC007622 AC007622 AC007622 AF011249 DRHOXA9 112149 AF011349 AF011349 AF011349 AF011349 AC04613 AC04617 AC04617 AC04617 AC04617 AC0608 HSJ65111 AC06210 HSJ65111 AC06210 HSJ65111 AC04617 AC06210	DNA t US 5686246.  G.W.  All-NOV-1997; Ilfiers  nknown 8 t
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KIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGODITDFTMQFVSS
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                     Erratum:[[published erratum appears in Nucleic Acids Res 1987 Jan
26;15(2):868]]
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 9721) Clark, B.D., Collins, K.L., Gandy, M.S., Webb, A.C. and Auron, P.E. Genomic sequence for human prointerleukin 1 beta: possible evolution from a reverse transcribed prointerleukin 1 alpha gene 87040762
   Gaps
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7275. .7405,8127. .8339)
7codon_start=1
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2291. 2297
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2458. 2465
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2466. 2527
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2006. .2465
   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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Human gene for prointerleukin 1 beta.
X04500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="G1:312408"
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   Mismatches
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                                                    1 GTTTAGGAATCTTCCCACTT 20
                                 1 GITTAGGAATCTTCCCACTT 20
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/number=2
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interleukin 1 beta.
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Bos taurus interleukin-1 beta (IL-1 beta) gene, 5' flanking region
and partial cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
Bovinae; Bos.
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                                                                                                                                         4274. 4279
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5125. 5326
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3092. .3143
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5874. :6038
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Pred. No. 1;
Mismatches 0;
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/note="pot polyA signal"
8931. 9721
/note="Alu repeat"
a 2328 c 2122 g 2608
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/note="inverted repeat A"
6213. .6220
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100.0%; Pr
tive 0;
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AF026543.1 GI:3258624
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                                                                               3144. .5124
                                                                                           /number=3
4266. .427
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7406. 812
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6039. .727
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Best Local Simila ity 100.
Matches 20, Conservative
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13356. .13480
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I (bases I to 139049)

S litren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P.,

Bairen, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P.,

Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R.,

Boutwell, C., Byrne, S., Cantu, C., Castle, A., Cerny, J., Cooke, P.,

Boutwell, C., Berreira, P., Forrest, C., Furke, R., Gaqe, D., Gardyna, S.,

Etemadis, S., Geraigery, K., Gilmartin, T., Gray, D., Hagos, B.,

Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Linton, L.,

MacKenzie, J., Marquis, N., McEwan, P., McGurk, A., Maldin, J., O'Connor, T.,

Molla, M., Morris, W., Morrow, J., Nachman, A., Naylor, J., O'Connor, T.,

Pavlin, B., Peterson, K., Ranganath, S., Riley, R., Roberts, D.,

Rollins, G., Rossello, R., Roy, A., Shyam, R., Soohoo, S.,

Stange-Thomann, N., Stilwell, J., Stone, C., Strickland, C., Sydney, K.,

Tang, L., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y.,
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                                                                                                                                     2 (bases 1 to 1895)
States, I.A.
Direct Submission
Submitted (24-SEP-1997) Comparative Biosciences, University of Wisconsin-Madison, 2015 Linden Drive West, Madison, WI 53706, USA 1. 1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 139049)
Birren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 17, clone CITI304117, complete sequence. AC004147
                 Tseng,Y.H. and Schuler,L.A.
Transcriptional regulation of interleukin-1beta gene by
interleukin-1beta itself is mediated in part by Oct-1 in thymic
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Unpublished
                                                                                                 Chem. 273 (20), 12633-12641 (1998)
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Pred. No. 59;
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90.0%;
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Best Local Similarity
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YEWNON, Zemicsava, I., Zhao, J. and Zody, M.

Direct Submission

AL Submitted (14-FEB-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases) 1to 139049)

Barren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Barren, B., Fasman, K., McKernan, K., Doepayre, E., Allen, M., Baker, J., Baldwin, J., Barnan, N., Beckerly, R., Benn, J., Boatin, C., Boutwell, C., Brown, A., Byrne, S., Cantu, C., Castle, A., Cerny, J., Cooke, P., Daly, M.J., Depayre, E., Devon, K., Fitzhugh, W., Forrest, C., Funke, R., Gaqe, D., Gardyna, S., Geraigery, K., Gilmartin, T., Grant, G., Gray, D., Ritzhugh, W., Forrest, C., Funke, R., Gaqe, D., Gardyna, S., Geraigery, K., Gilmartin, T., Grant, G., Gray, D., Rann, L., Linton, L., Maddonald, P., Marquis, N., McEwan, P., McCurk, A., Maloria, J., Wolla, M., Morris, W., Morrow, J., Nachman, R., Nahf, R., Roberts, D., Rollins, G., Rosello, R., Roy, A., Shyam, R., Stange-Thomann, N., Stilwell, J., Stone, C., Strickland, C., Stoney, K., Tang, L., Vassiliev, H., Vo, A., Wagner, A., Shomey, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and Zody, M.

Direct Submission

AL Submitted (28-Mar, 1998) Whitehead Institute/MIT Center for Genome Research, 330 Charles Street, Cambridge, MA 02141, USA on Mar 28, 1998 this sequence version replaced gi:2967619.

All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker:html.
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Ye, W.J., Zemtseva, I., Zhao, J. and Zody, M.
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/rpt_family="(CA)n"
12493. 12724
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/rpt_family="MIR"
4324. .4542
/rpt_family="MER20"
complement(5646. .5803)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .139049
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="LINE2"
539. 9610
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complement(2984. .3179)
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1290, 1413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416. .439
/rpt_family="AT_rich"
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complement(9161. .9.
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11072. .11227
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/rpt_family="MIR"
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/rpt_family-"MIR"
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t_family=" plement(15	family="(CA)n 118719	.(19314 .'(19314 .'="AT	6		0804.	/rpc_ruminy	/ipt_lamily="Alubb" 2224722279 /art family="Alubb"	/rpt_ramily="(GAAAA)n" 2230222324	/rpt_family="AT_rich" 2405724121	/rpt_family="MIR" complement(2428324316)	tamily="(TAAA) 24977	family="LTR 26784	1 (1)	27385 27385	-"MST 27752	="MSTC" 2804328164	, Z	y-"LINE2 (29966.	amily="L1MC4	(33029.	33 33 34 35	34560	manly="MER4D ement(35177	- MER4D 78	maily="Ar_rich ement(357493	ement(37344.	39153	_tamily="LTR12 lement(39154.	ement(40534.	40883	rpt_family="LIM 208042224		family="ME ement(4277	family-"MIR ement(43354	MER
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Submitted (09-Aug-1996) Louis, MO 63110, USA. E-mail:
Submitted (09-Aug-1996) Louis, MO 63110, USA. E-mail:
Jesésanger.ac.uk or rwénematode.wustl.edu
2 (Dasses 1 to 42042)
Rilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Button,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du.Z., Durbin,R., Faveilo,A.,
Fulton,L., Gardner,A., Green,P., Hankins,T., Hiller,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rikken,L., Sonnhammer,E.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Thlerry Mieg,J., Thomas,K., Vaudin,M.,
Wilkinson-Sproat,J. and Wohldman,P.
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Caenorhabditis elegans
Eukaryota; Metazoa, Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 42042)
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94150718
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.

The sequence and its analysis sequence and its analysis see:
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complement(47626. .4771)
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complement(47106. 47146)
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/rpt_family="MIR"
complement(47250
/rpt_family="MIR"
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complement(51018. .51119)
                                                                                                                                                                                                                                                             /rpt_family="Line2"
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complement(50630..50798)
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complement(49715.
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CEC34B4/c
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Homo sapiens 12p13 BAC RPC111-154121 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDKVVYSEIVKHRSTEKEYLPALPSHOPRQWENRLIGAAEKCLSVIDGADSEGTSTGP
SVSPYHVSDVSRISSNNRTESPGSRKSSKLSRNSSPRVPSHHSYEDGAAYAIRDLCLG
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OISFYRALNRDEEPASKISIBLRSVYFDIDASISGWLTRVKCGLSKKVFAALVNOKLMFFK
NSNDLVPNGFLCLQGAQISEKHNGTEEYSGSSDEQLETTKEHPNGPKNNDSLCVQIAN
LEFTATSEDKEKMYTYTKASAGTAALCOFPEILQKMAAENVANMIFHNEDR
LEFTATSSDFEKEMLYTYTKASAGTAALCOFPEILQKMAAENVANMIFHNEDR
TQYHIDDAQNILSTAVQOEYLANESDETRMAIFCESALDRCLRVGGROEGFSRLEVTS
VLIRDVTRKRPPHSISVKLPNSEYQIVEFOGGKLCCALSFTFTRSDAQRRRVISDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAALSLRMRHYWGHLALTETP IERÔFLVWRASËEI VNGR I PLSNOLCESLAALYAOWY
SCRÄNGSLSDOOFEET SORFYPSKMLDVACT KSLILQI NSWWSELIORBENECYRVIL
GVLGKWPLFGSDLHASMRTDNERT YT LALDHSVSLLIDRRHFDVI RTI PYSSLSTFG
GFQQDFMLTI IIRPLFPGSHPDEAPKERLIFSMOKNEI EQLI LHLAEY I RCOK I VWRVS
comes from this gene; cDNA EST EMBL:D36335 comes from this gene; cDNA EST EMBL:D67933 comes from this gene; cDNA EST Y260h6.3 comes from this gene; cDNA EST Y8260h6.5 comes from this gene; cDNA EST Y8243d7.3 comes from this gene; cDNA EST Y8243d7.3 comes from this gene; cDNA EST Y8243d8.5 comes from this gene; cDNA EST Y8249d8.5 comes from this gene; cDNA EST Y8209h12.3 comes from this gene; cDNA EST Y8209h12.5 comes from this gene; cDNA EST Y8209h12.5 comes from this gene;
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LPRRIHPTATERDSLNSTAEDYEYDIEESSFERHEEQVRNENEKYUDYVNLHEEVAIK
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 161348)
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Direct Submission
Submitted (13-MAY-1999) Molecular and Human Genetics, Baylor
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90.0%; Pred. No. 38;
iive 0; Mismatches 2;
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2 (bases 1 to 161348)
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AC007535.2 GI:4914349
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                                      bin/displaydb=wormace&class_Sequence &object=C14B4
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

In PORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because (1. 101) overlaps with the end of clone F42EB is at 18123 in this sequence 283242.

The end of this sequence (41942. .42042) overlaps with the start of sequence 283242.
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TLNIVFNVPARLESYATEQPYIXIMLYMIYVLPSLTLIFLGODNCMYRFDNRECKFTL
TCNIVGTNKVKIEIPRIIQIIEDTIQIIDTILIILIILXIALVIKIIKMKTSRNKTEI
IILKQAFFIFELMFOTYNIIVLYGKTLKMTYTVAFYLKRAIHTAEIFAGATTPCFFYFT
SKEIKKLVSNKITAGSOGNSVLRNIASVPRNS
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KKRLYALPPDFAATGYTSNNLMAPPDHESCHBPETSPESGTSSLFSPFDMM
SMFPDPTRPTVSDDRMAPPAATVRKNVVRRRPRECSMVCWLFRTLLTSEYRALPANA
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EST EMBL:D33476 comes from this gene; cDNA EST EMBL:T00122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted using Genefinder; similar to Activin
types I and II receptor domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis elegans"
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/chromosome="V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref-"SPTREMBL:Q18419"
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/db_xref="GI:3874640"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13357. .28308
/gene="C34B4.2"
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gene CDS

gene

FEATURES

CDS

Direct Submission

Worley, K.C.

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

AUTHORS TITLE REFERENCE

JOURNAL

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atgaítatca(t)tgttattatt
attctcaaag(g)agtgataatg
tctcaaagga(g)tgataatggg
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ctttcatccc(c)acttttgggg
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tgccatgtct(c)ttcaagtcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                  aaaagatttt(t)tgtttccacg
atacata'.t(t)atttgctttt
atttgcttt(t)ttttttttt
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tttggaagct(t)ttatttactt
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actatcactc(a)cccggtcttc
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ggttggtggag(a)attttccagt
gttggtggag(a)ttttccagtt
aacatttaaa(a)acatacatat
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                                                               tctcataact(c)atcttactgg
aactcatctt(a)ctggataaat
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gtgttgacat(t)ttaagtaagg
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Phrap Value Range
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tttggaagct(n)ttatttactt
agagagagg(n)ctttcaagac
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gactatcant(n)ncccggtctt
actatcantn(n)cccggtcttc
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aacatttaaa(n)acatacatat
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aaaagatttt(n)tgtttccacg
atacatattt(n)atttgctttt
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caaaaacaan(n)gacccagaat
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actccagcca(n)agaccactca
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Location/Qualifiers
1. .161348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
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112343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                       CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Peports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
                                                                                                                                                                                                                              Submitted (29-MAY-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 28, 1999 this sequence version replaced gi:4809319.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggaaactgca(a)ccttaagcga
tgtgaaata(g)acagattgac
tgacagattg(a)cagcccttag
atggtgtgag(a)catcactgag
tgtccattat(c)tatttagatt
tttctctgta(a)tctttcctt
                                                                           Direct Submission
Submitted (28-MAY-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 161348)
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160601
0.000327607
0.038275
       One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus changing edits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Average error rate (BCM-Phrap estimate):
Faction of Phrap values less than 40 :
Number of consensus changing edits:
Number of N's in consensus :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      figuaaata(n)acagattinc
tnacagattg(n)cagcccttag
atgitytgag(n)catcactgag
tgccatta(n)tatttagatt
tttctctgta(n)tttttcctt
ttttatattt(n)gaaattatta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANNOTATION OF FEATURES:
                                 (bases 1 to 161348)
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Contig length:

Position 15946 20708 30717 39533 51460 52928 52994

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/note="Overlaps with bases 1-226 in AC002996."
/note="Region: Overlap with AC002996"
join(88. 201,843. 945,1380. .1564,6860. .7024,8688. .8845,12611. 12755,18325. .18759)
/gene="Human nucleus-encoded mitochondrial aldehyde dehydrogenase(ALDH)gene"
                                                                                                                                                                                                Direct Submission Submitted (17-SEP-1998) Human Genome Sequencing Center, Department Submitted (17-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 31, 1998 this sequence version replaced gi:2909690. Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.

Location/Qualifiers
1. .139166
                                                                          Submitted (16-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 139166) Welley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence similarities were identified using Powerblast by Jinghui
                                                                                                                                                                                                                                                                                                                                                                                                                                           The repeat regions shown were identified using RepeatMasker by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hs.74630, K03001, X05409*
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 139166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(4069...4364)
/rpt_family="Alusx"
complement(4374...4672)
/rpt_family="Alusg"
4761...4893
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/rpt_family="LIMC2"
complement(3291. 3588)
/rpt_family="Aluco"
complement(3608. 4064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RPCI3-462E2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="LIMC2"
ement(2800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="FRAM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2260. .2370) /rpt_family="LiMC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2374. .2612) /rpt_family="Alusx"
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/rpt_family="AluJb"
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                                           Worley, K.C.
Direct Submission
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 139166)

Muzny, D., Arenson, A.D., Adams, C., Bunac, C., Carvelli, K., Chang, J., Chacko, J., Chen, J., Diag, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Garcia, C., Goodman, M., Gorrell, J., Haywood, M., Hernandez, J., Jackson, L., Jin, S., Kampal, R., Haywood, M., Lau, S., Leal, B., Lee, E., Li, Y., Lichtarge, O., Liu, W., Logan, O., Lu, J., Ly, T., Marchdel, I., Martinez, C., Merscher, S., Montgomery, K., Oswal, G., Penez, L., Rashid, N.D., Renault, B., Rowland, K., Savage, L., Scher, H., Simon, M., Stovall, K., Timms, K.M., Todd, J., Nelson, D. and Gibbs, R.A.

I Unpublished
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Submitted (31-JUL-1998) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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Homo sapiens Chromosome 12q24 PAC RPCI3-462E2 (Roswell Park Cancer
Institute Human PAC library) complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.0%; Pred. nv.
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complement(14494. .14543)
/rpt_family="(TA)n"
14626. .14720
                                                                                                                                                                                                                                                                                                          rpt_family="MLT1F"
314. 9606
                                                                                                                                                                                                                           complement(4368. .4503)
/rpt_family="MIR"
7912. .8298
                                              /clone-"RPCI11-154121"
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0218. .10515
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                                                                     /chromosome="12p13"
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14797. .14843
                                                                                                                                      156. .530
/rpt_family="MIR"
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15478. .15607
                                                                                                                 'rpt_family""L2"
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AC003029.1 GI:3366554
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Best Local Similarity 90.0
Matches 18; Conservative
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Waterston, R. H.
Direct Submission

Waterston, R. H.
Direct Submission

Submitted (16-ARR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

On Jun 5, 1999 this sequence version replaced gi:4586090.

* NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces.

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as trus of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
n 17954. .18213

'rpt_family="AluJo"

18511. .186213.

18511. .18612. .18612.

'gene="Human nucleus-encoded mitochondrial aldehyde

'gene="Human nucleus-encoded mitochondrial aldehyde

'gene="Human nucleus-encoded mitochondrial aldehyde

| gene="Human nucleus-encoded mitochondrial aldehyde

| gene="Human nucleus-encoded" | gene="Human nucleus" | gene="Human nucleus
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Homo sapiens clone NH0356B17, WORKING DRAFT SEQUENCE, 4 unordered
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180549)
Waterston,R.H.
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36197 36214: gap of unknown length
36215 74570: contig of 38356 bp in length
74571 74588: gap of unknown length
74589 124355: contig of 49767 bp in length
124356 124373: gap of unknown length
124374 180549: contig of 56176 bp in length.
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Pred. No. 52;
0; Mismatches
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1. .180549
/organism="Homo sapiens"
/db_xref="taxon:9606"
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g5001505
AC007316.2 GI:5001505
HTG; HTGS_PHASE1.
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Best Local Similarity 94.4%;
Matches 17; Conservative
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standard_name="DWC10/DWC11"
note="GDB:179565, Chr. 12q24.2-1-2q24.2, Homo Sapiens"
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complement(16333. .16541)
/rpt_family="L2"
complement(16588. .16956)
/rpt_family="Alusx"
1692. .17186
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complement(13595. .13622)
/rpt_family="AT_rich"
13999. .14103
                                                                                                                                                                                                                                                                                                                                                        complement(9202...433)
/rpt_family="AluJo"
/rpt_family="LIMB6"
/rpt_family="LIMB6"
complement(9788...10134)
/rpt_family="THE1B"
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complement(14148. .14404)
/rpt_family="AluJb"
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complement(17550 .17928)
/rpt_family="L2"
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complement(12530. 12557)
/rpt_family="AT_rich"
                                                                                                                                                                                 /rpt_family="AluSx"
complement(7800. .7943)
/rpt_family="AluSg"
complement(7947. .8248)
/rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                      /rpt_family="FLAM_C"
complement(9202
                                                     6185. .6402
/rpt_family="AluSg/x"
complement(7325. .7487)
/rpt_family="FRAM"
       complement(5744. .6014)
/rpt_family="AluSg"
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1996. .12094
pt_family="(TAAAA)n"
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/rpt_family="Alusc"
10918. 1171
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/rpt_family="LIMB6"
10755. .1001
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/rpt_family="Alusc"
14814. .15118
/rpt_family="Alux"
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7205. 17505
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rpt_family="Alusx"
5767. .16064
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0201. .10493
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rpt_family="AluSg"
1214. .11379
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1693. .11988
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/db_xref="Ci:1029970"
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KRNDDRVKRPNNAFMWSRGQRKKMALENPKMHNSEISKRLGTEWRMLSEQEKRPFID
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QYIDGFRFAPYPTTYMDQIPFSTYPHSPROAPTDNSSPSQFQPSPWSTTTTYMNATN
QXIDGFRFAPYPTTYWDQIPFSTYPHTKGINKTPSPSTFTTTTYMOTIPFSTYPHTKGINGYPTSPSSPSGFGGPSPWSYLTFR
COMPLement(1818 .27091)
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AKCSRCGCVAMFYADFVLSKKGPLSKVWLAAHWEKKLSKADIFETDVDEAVNEIMOP
SQKLALRTIGHLLLGICRVYSKRYKYLLADCNEAFLKIKLVFRSGALDQPNPVLPTFS
IQDIYGGFGDNVLPFEFDEELNHAPTCQSRLDDITLKEDIPCKFTYRYGEPLEDDDFG
EIAAGVGFEDYYRLMEDVNKMDLEMELARDAATTSDNLFGREREFTFFLNDAHAPGNA
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FERMSBAPPSTAFBVSTARBYSARHDTITESYYEROGYRAMQK ROMRKRENGDNRKRYENDDVWHTG
FERMKGNMADFSDLIAFDSRKLAMGKRESHAEVMHHNCGMIGFSKNKOFTRG
SYLVVTKHDDVDEKNEWIKNALGLREIGEEELQQQQCEMDMHVQDDSSYVDDFDEVPP
LEDFOLLDMONPQSMDDINWYDDDVPORNPLSPFAPWYEDEEMSPSSKRKRRDEEKEE
PETDEDNRASKRTHALLQNIATKLENQNGQVELDEMLKKGTSRKVAAAKFYSELLCLKK
NQCIDIEQKEPYGDIMIKAGPNINITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(18118. .18288,19895. .19999,20892. .21092, 22889. .23029,23078. .23210,24517. .25085,26088. .26237, 26429. .26608,26665. .26809,26928. .27091))
// gene="Wcodas." a miniarity to M. musculus ubiquitin carboxyl-terminal hydrolase (SP:UBP_MOUSE, P35123); Similar to S. pombe double-strand-break repair protein, RAD21 (SP:RAZ1_SCHPO,P30776); coded for by C. elegans cDNA CEESR77F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA79746.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQPIPERIIGKLSVSIIKALHYLKTKHQIMHRDVKPSNILLDWSGVIKLCDFGIAGRL
IESRAHSKQAGCPLYMGPERLDPNNFDSYDIRSDVWSFGVTLVELATGQYPYAGTEFD
MMSKILNDEPPRLDPAKFSPDFCQLVESCLQRDPTMRPNYDMLLQHPFVVHHEKIETD
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ERRANIEMEEQYRADKREQEQAKEFEDLQHRRESVSQINQSRRGTTQILARGNEVS
INGETWCQLPPHHPIPAIISDRSQYSQRIGRDRVSRLIIGFCSKTKLIKCKNRR"
6242 c 6369 g 10710 t
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RTSNSYEMSRILMDLDVICLSFDCPYIVRCFGYFITNFDVRVCMECMATCLDRLLIRI
                                                                                                                                                                                   complement(join(10814. .11194,11247. .11351,11423. .11548,
11990. .12053,12132. .12280))
/qene="K0848.2"
/note="K0848.2"
/note="similar to mammalian sex-determining protein SRY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coded for by C.
elegans cDNA cm04a9"
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32206. 32366,33479. 33583,33626. 33830,33875. 34048)
/gene="KOBAB.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"similar to map kinase kinases;
elegans cDNA cm14d12; coded for by C.
                         organism-"Caenorhabditis elegans"
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                                                                                                                                complement(10814. .12280)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAA79748.1"
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/db_xref="G1:1022971"
                                          /db_xref="taxon:6239
                                                                                                      /strain-"Bristol N2"
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/gene-"K08A8.1"
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Caenorhabditis elegans

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;

Rhabdituna; Rhabditiodea; Rhabditidae; Peloderinae; Caenorhabditis.

I (bases 1 to 3447)

Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,

Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,

Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,

Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,

Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,

Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,

Saunders, D., Shownkeen, R., Sanaldon, N., Smith, A., Sonnhammer, E.,

Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,

Wilkinson-Sproat, J. and Wohldman, P.,

2. Mb of contiguous nucleotide sequence from chromosome III of C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Genetics, Washington University, St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        19-0CT-1995
                                                                                                                                Length 180549;
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                                                                                                                                     DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CELKOBAB 34347 bp DNA Caenorhabditis elegans cosmid KOBAB. U38377
                                                                                                                                Score 16.4; Di
Pred. No. 50;
0; Mismatches
                         54456
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Nature 368 (6466), 32-38 (1994)
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/clone="NH0356B17"
36172 c 35964 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (11-OCT-1995)
Submitted by:
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                                                                                                                                                                                                                                                                           4556 TTTAGGAATCTTCCCATT 4573
                                                                                                                                     82.0%;
94.4%;
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Submitted (11-OCT
                                                                                                                                                                                           Conservative
                                                                                                                                     Query Match
Best Local Similarity
Matches 17; Conserv
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U38377.1
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ACCESSION
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ORIGIN
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TITLE
JOURNAL
REFERENCE
AUTHORS
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JOURNAL
COMMENT
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MEDLINE
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SOURCE
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us-09-037-472-4.rge

LOCUS

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Potatoe; Lycopersicon.
1 (bases 1 to 51953)
Rossi,M., Goggin,F.L., Milligan,S.B., Kaloshian,I., Ullman,D.E. and
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3 (bases 1 to 51953)
Bodeau, J.P., Kaloshian, I., Milligan, S. and Williamson, V.M.
Direct Submission
Submitted (07-DEC-1996) Nematology, CEPRAP, 1930 5th St., Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon esculentum subaryophyta; Embryophyta; Tracheophyta; bukaryota; Viridiplantae; Streptophyta; Embryophyta; eudicotyledons; core euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEU081378 51953 bp DNA 19-AUG-1998 Lycopersion esculentum disease resistance gene homolog Mi-copy? Gene, complete cds; resistance gene pseudogene, complete squence; disease resistance gene homolog Mi-copyl gene, complete cds; and
Direct Submission
Submitted (31-JUL-1996) CEPRAP/Nematology, Univ.California, 1930
5th St., Davis, CA 95616, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1. .1055)
/note="similar to Smcy/Retinoblastoma binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bodeau, J.P., Kaloshián, I., Milligan, S. and Williamson, V.M. Isolation and large-scale sequencing of bacterial artificial chromosomes (BACs) spanning the tomato Mil nematode-resistance
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williamson, V.M. Statement of toward confers resistance against the potato aphid against the potato aphid 98374252
                                                                                                                                                                         /mapa"Between GP79 and APS1"
2865. .6483
/note="putative Mil gene; encodes putative nematode-resistance gene; Allele: R; exon/intron boundaries are not known"
a 1070 c 1262 g 2439 t
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                                                                                                                                                                                                                                                                                                                                                       Length 6999;
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1. .191953
...organism="Lycopersicon esculentum"
/cultivar="Motelle"
                                                                                                    esculentum"
                                                                                                                                                                                                                                                                                                                                                       80.0%; Score 16; DB 8; Le
100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map-"between APS and GP79"
                                                                           1. 6999
/organism="Lycopersicon e
/strain="Motelle"
/db_xref="taxon:4081"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4081"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16312. .19932
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U81378.1 GI:3426259
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                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TTTAGGAATCTTCCCA 17
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: rore
euphyllophytes: Spermatophyta: Magnoliophyta: eudicotyledons; core
eudicots: Asteridae: euasterids I; Solanales; Solanaceae: Solanum;
Potatoe: Lycopersicon.
I (bases 1 to 6999)
Williamson, V.M., Bodeau, J.P., Kaloshian, I., Yaghoobi, J. and
Milliamson, S.
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(Dases I to 80858)

Waterston, R.H.
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Lycopersicon esculentum putative Mil copy 2 nematode-resistance
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On Jun S, 1999 this sequence version replaced g1:4662676.
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Homo sapiens clone NH0104K07, complete sequence.
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/organism="Homo sapiens"
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/clone="NH0104K07"
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        ed. No. 63;
Mismatches
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Unpublished
          Pred. No.
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Waterston, R.H.
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LIPLQEHNYTVITPSTSGARNIHVNMEFLLLILSDMRKDFIHHDKLFDLLDRVGVLTR
SYSTUKNDLEEEPRNKEGNNOTNCATLDLLENIELKKDLKHVYLKALDSSQCCFPMS
DGPLFMHLLHIHLNDLLDSNAYSIALIKEFIELVKQDLKFIRSFFVDAEQGLYKDLWA
RVLDVAXTEARDVIDSIVRDNGLLHLFSLEPTTIKKIKLIKERISALDENIPRORGLI
VVNSPKRPVERKSLTIDKITVGFEEETNLLILRKLTSGSADLDVISITGMPGSGKTTLA
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LEGKRYLLIVDDWDTTTWDDELTRPPESKKGSRILITTREKVALHGKLNTDPDLDLR
LLRPDESWELLEKRAFGURSCPDELLDVGKEIAENCKGLPIVADLIAGVIAGREKKS
VWLEVQSSLSSFILNSEVEVWKVIELSYDHLPHHLKPCLLYFASFPKDTSLTIYELNV
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LETELSVGFKGSNTNDSGSSYATNRPWDPFPSPNKTLIWLREFPLTSDSLSTARLPNL
EELSLYTTIHGESWNMGEEDFFENKFLNROVSISKWEVGEESFPNLEKLKRGCH
KLEEIPPSFGDIYSLKSIKIYKSPQLEDSALKIKEYABDMRGGDELQILGQKNIPLFK
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ARVLDVATREAKUVIDLUDSNAY SISLIKEEIELVSQELEFIRSFEGDAAGGLYKDIM
ARVLDVATREAKUVIDLUDSNAY SISLIKEEIELVSQELEFIRSFEGDAAGGLYKDIM
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RLLRPDESWELLERRFEGNESCPDELLDVGREIAENOKGLPLVADLIAGVIAGREKKR
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KYLAGGEVEKTEMKGIEEVWKIVIELSYDHIPHHLRCLLHFASWPRDTPLTITLIT
KARKENLEDR RRSSASSDLLPRQITIDYDEEEBHFGLNFVWEDSINKRHSGKHLYSLR
INGDQLDDSVSDAFHHRLRLIRIVLDLEPSLINVUSSLLNEICHINTERIKTIRIV
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CGNIRDFHGLIVNGCIKHEMVENVLPLFQLMADRVGHFLMDDQTDEDSRLSELDEDEQ
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GDQLDDSVSDAFHLRHLRLLRVLDLHTSFIMVKDSLLNEICMLNHLRYLSIDTQVKYL
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TELETLCVGFKSSNTNHCGSSVATNRPWDFHFPSNLKELLLYDFPLTSDSLSTIARLP
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GGNIRDFHGLILLNGCIKHEMVENVLPLFQLMAERVGHFLWEDQTDEDSRLSELDEDEH
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EVSTLVRDLEEKLRNKEGNNQTNCATLDLLENIELLKKDLKHVYLKAPNSSOCCFPMS
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CDS

CDS

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Direct Submission
Submitted (16-NOV-1995) U. Arnason, Dept of Genetics, Division
Evolutionary Molec. Systematics, University of Lund, Solvegatan 29,
S-223 62 LUND, SWEDEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12S ribosomal RNA; 12S rRNA gene; 16S ribosomal RNA; 16S rRNA gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COI gene; COII gene; COIII gene; CONTROL region; Cytb gene; NADH1 gene; NADH2 gene; NADH3 gene; NADH4 gene; NADH4 gene; NADH5 gene; NADH6 gene; NADH6; transfer RNA-Asn; transfer RNA-Asn; transfer RNA-Clu; transfer RNA-Glu; transfer RNA-Lys; transfer RNA-H1s; transfer RNA-Lys; transfer RNA-Lys; transfer RNA-Lys; transfer RNA-Yer; transfer RNA-Thr; transfer RNA-Try; transfer RNA-Tyr; transfer RNA-Tyr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu,\dot{X}. and Arnason,U. A complete sequence of the Mestern A complete sequence of the mitochondrial genome of the Western
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gorilla.
Mitochondrion Gorilla gorilla
Eukaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrini; Hominidae; Gorilla.
1 (bases 1 to 16412)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                           ö
complement(49849. .50313)
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                                                                                                                                                                                                                                                                                                                           Length 51953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMITG 16412 bp DNA PRI genome.
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                                                                                                                                                                                                                                                                                                                      DB
97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 16412
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1091. .2648
                                                                                                                                                                                                                                                                                                                           Score 16; DB 8; Pred. No. 97; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product="transfer RNA-Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mitochondrion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 14096 TTTAGGAATCTTCCCA 14111
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Best Local Similarity 100.
Matches 16; Conservative
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rRNA

us-09-037-472-4.rge

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5 943689
D38114.1 GI:643689
Subunit I: Nable dehydrogenase
Subunit I: Nable dehydrogenase subunit 4: Nable dehydrogenase subunit 4: Nable dehydrogenase subunit 4: Subunit I: Nable dehydrogenase subunit 6: Cytochrome b: Cytochrome c oxidase subunit II: Chan-Lis; tRNA-Lis; tRNA-Lis; tRNA-Lis; tRNA-Lis; tRNA-Lis; tRNA-Tyr; tRNA-Tyr; tRNA-Val. Gorilla gorilla mitochondrion Gorilla Goril
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Gorilla mitochondrial DNA, comlete sequence.
D38114
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Best Local Similarity 100.
Matches 16; Conservative
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GORWIC/C
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DEFINITION
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KEYWORDS
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REFERENCE

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8629. .9411
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                complement(6866. .6937)
/product="tRNA-Ser(UCN)"
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/product="tRNA-Ser(AGY)"
111688. .11758
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/product="tRNA-Lys"
7788. .7994
/codon_start=1
                                                  6939. .7006
/product="tRNA-Asp"
7007. .7600
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9481. .9825
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9892. .10188
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11629. .11687
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/codon_start=1
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                   Direct Submission
Submitted (O2-SEP-1994) to the DDBJ/EMBL/GenBank databases. Renji
Hayasaka, National Institute of Genetics, Human Genetics; 1,111
Yata, Mishima, Shizuoka 411, Japan (E-mail:khayasak@dbj.nig.ac.jp,
2 (sites)
2 (sites)
A comparison of the small ribosomal RNA genes from the
mitochondrial DNA of the great apes and humans: sequence,
structure, evolution, and phylogenetic implications
Mol. Biol. Evol. 3 (1), 1-18 (1986)
                                                                                                                                                                                                                                                                                                                                                                       Foran, D.R., Hixson, J.E. and Brown, W.M. Comparisons of ape and human sequences that regulate mitochondrial DNA transcription and D-loop DNA synthesis Nucleic Acids Res. 16 (13), 5841-5861 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Man's place in Hominoidea revealed by mitochondrial DNA genealogy
J. Mol. Evol. 35 (1), 32-43 (1992)
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Horai,S., Satta,Y., Hayasaka,K., Kondo,R., Inoue,T., Ishida,T.,
Hayashi,S. and Takahata,N.
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Horai,S., Hayasaka,K., Kondo,R., Tsugane,K. and Takahata,N.
Recent African origin of modern humans revealed by complete
sequences of hominoid mitochondrial DNAs
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/product="tRNA-Tyr"
5325. .6863
/product="cytochrome c oxidase subunit 1 (COI)"
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Unpublished (1995)
Location/Qualifiers
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/product="NADH dehydrogenase subunit 1 (ND1)"
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/Product="NADH dehydrogenase subunit 2 (ND2)"
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?product="tRNA-Leu(UUR)"
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complement(3747. .3818)
/product-"tRNA-Gln"
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/product="tRNA-Cys"
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/product="tRNA-Ala"
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/product="12S rRNA"
1021. .1089
/product="tRNA-Val"
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/product="16s rRNA"
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3888. .4928
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  Hayasaka, K.
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Homo sapiens chromosome 3 clone pDJ70111, WORKING DRAFT SEQUENCE, 2
unordered pieces.
                                                                                                                                                                                                       /codon_start=1
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/protein_id="BAA07307.1"
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/db_xref="PID:q1213359"
/db_xref="TID:q1213359"
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I (bases I to 164296)

Evans, G.A., Bradbury, P., Brignac, S., Bumeister, R., Davie, J., Davies, C.J., Davis, C., English, C., Fondon, T., Franklin, T.L., Garner, H.R., Gordon, M., Gotway, G., Grant, O., Hahner, L., Harris, J., Oliver, T., Patel, P., Probst, S., Rayner, S., Schageman, J., Schilling, P., Schultz, R., Syed, M., Valenzuela, D., Ward, T., Mard, T., Silson, R. and Burbee, D.
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Evans, G.A., Bradbury, P., Brignac, S., Bumeister, R., Davie, J.,
Bavies, C.J., Davis, C., English, C., Fondon, T., Franklin, T.L.,
Garner, H.R., Gordon, M., Gotway, G., Grant, O., Hahner, L., Harris, J.,
Hinson, S., Megarity, C., Narayanaswamy, U., Newton, J., O'Brien, K.,
Schilling, P., Schulz, R., Syed, M., Valenzuela, D., Ward, T.,
Wilson, R., and Burbee, D.
LNPIKRLTIGSLFAGFFITNNILPTSVPQMTIPLYKLTALSITLLGLLTALDINYLT WIKKKHYPHPTFYFSNMLGFFVNITHRTIPYLGLLMSQNLPLLLLDLTMLEKLLPKTI SQHQISASITTSTQKGLIKLYFLFFFPLLLILLIT" COMPLEMENT (1371. 14095)
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Pred. No. 1.1e+02;
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/product="tRNA-Pro"
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/product="tRNA-Gln"
14169. .15308
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15310. .15377
/product="tRNA-Thr"
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HTG; HTGS_PHASE1.
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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September 18, 1999, 05:27:18; Search time 213.04 Seconds (without alignments) 23.488 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-037-472-4 20 1 GITTAGGAATCTTCCCACTT 20 Title: Perfect score: Sequence:

Scoring table: IDENTITY\_NUC Searched:

311585 seqs, 125096042 residues N\_Geneseq\_36:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description		Primer for detecti		rimer used t	leukin 1 (44	IL-1ra BAC	n IL-1ra	omato Mi	Mi resis	ato pest re	id pTM72	low Km,	d pTM72 (A	vacuolar i	vacuolar i	vacuol	acid	omato acid inv	a	cid	rabidopsis th	3	ccus fae	ರ	æ	cine pro-inter	cipa		eb1-2	₫	ain am	lysi	elic	apoptosi	ine HIAP-1 co	DG17.	nce of AR	ι temporal	associa	ssoci	of	e of hum	_	viral
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Ę	1	T138	V32	V60	X16	X22	X02	V16	V13	V26	014	071	T34	028	028	028	039	063	094	TOI	V34	V74	X12	<b>X</b> 20	V21	073	083	T23	T72	T72	T98	667	X12	T70	V55	۸	N60	014	014	014	N4 O	N40	025	031
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ALIGNMENTS  SSULT 1  SSULT 1  SALIGNMENTS  ALIGNMENTS  SCOLT-1997 (first entry) 19-007-1997 (fir	). primer; amplificati ; interleukin-1-alpl s.
standard;  standard;  standard;  for detection of the secondard;  sase chain all assection of the secondard;  KORNMAN;  MEDICAL:  1995; U12-  1996; U1	T 2  92392 standard; DNA; 20 BP.  932392; 11-SEP-1998 (first entry) Interleukin-1-beta primer 2 (-417/-398).  11-1-beta; genetic polymorphism; PCR; primer; amplification; sight threatening diabetic retinopathy; interleukin-1-alpha; interleukin-1-beta; interleukin-1RN; ss.  10-10-1996; GB-02129.  10-CCT-1997; G02790.  10-CCT-1997; G02790.  10-CCT-1997; G02790.  10-CCT-1997; GB-021129.  (RENN/) RENNIE I.  (RICH/) RICHARDSON R.  Duff G, Rennie I. Richardson R;  WPI; 98-240835/21.
RESULT 1 11386 standard; DI 119-CCT-1997 (firs) 10 T1386; DI 10 T1386 standard; DI 10 F1900 (firs) 10 F1900 (firs) 10 F1900 (firs) 10 F190 (firs) 11 F1	RESULT 2 V32392 AC V32392 DT 11-SEP-198 ( DE Interleukin-1- KW Interleukin-1- KW Sight threaten KW ANDELLAND SIGHT ( SON HOME SAPINS PD 16-ARR-1998 ( DE 100-CT-1997; G PR (00-CT-1997; G PR (00-CT-1997; G PR (100FY) RENNIE PR (100FY) RENNIE PR (100FY) RICHAR PI MPI; 98-240835

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1 GTTTAGGAATCTTCCCACTT
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                                                         Symptoms occur.

Claim 2; Page 33: 41pp; English.

Claim 2; Page 33: 41pp; English.

Interleukin-1-beta (IL-1-beta) primers 2 and 1 (V32391) were used to amplify the IL-1-beta gene region to identify single base variation polymorphism of c/T at base 51.

The invention claims to provide a method involves isolating DNA from a patient and determining the DNA polymorphism pattern of the genes that code for interleukin-1-alpha, interleukin-1-beta and interleukin-1RN. The polymorphism pattern compared with controls of known DNA polymorphism patterns thereby identifying patients carrying a genetic polymorphism patterns thereby identifying patients carrying a genetic polymorphism associated with increased risk of sight threatening diabetic retinopathy. The method may be able to identify diabetic patients at risk before the clinically detectable disorders occur. Polymorphism pattern clinically detectable disorders occur. Polymorphism pattern in genome involved PCR reactions using primers v32389-v32389. The method is also claimed to be useful in conjunction with identification of other genes associated with sight threatening diabetic retinopathy in genomic DNA and therefore, in identifying diabetic
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PCR primers V6032-33 were used to amplify alleles associated with interleukin-lb (IL-1B). The specification describes a method for determination of a patient's predisposition to coronary artery disease. The method comprises comparing an allele with a second allele which is predictive of coronary artery disease, where similarity between the first and second alleles indicates a predisposition to coronary artery disease. The method is used to genotype an individual's interleukin (IL)-ll loci, the method is used to screen a patients' predisposition to coronary artery disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of predisposition to coronary artery disease - by comparative measurement of levels of expression of alleles from the interleukin 1 locus
 Predicting increased risk of sight-threatening diabetic retinopathy
                comprises identifying genetic polymorphism pattern for genes ,-1A, IL-1B and IL-1RN, useful to allow treatment before clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-NOV-1998 (first entry)
PCR primer used to amplify interleukin-1B (IL-1B).
Interleukin-1B; IL-1B; predisposition; coronary artery disease;
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                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 0.23;
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                                                                                                                                                                                                                                                                                                                                        patients expressing multiple risk patterns.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-1998; U04725.
10-MAR-1997; US-813456.
MbDI-) MBDICAL SCI SYSTEMS INC.
Crossman DC, Duff GW, Francis SE;
WPI; 98-520829/44.
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100.08; P1.
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                                                    symptoms occur
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WPI: 99-080814/07.

Prov method of determining a patient's susceptibility to inflammatory of sorders - by detecting the presence of an IL-1 (4411232)

Proporders - by detecting the presence of an IL-1 (4411232)

Proporders - by detecting the presence of an IL-1 (4411232)

Proporders - by detecting the presence of an IL-1 gene cluster

Claim 3: Page 33: 49pp; Engdish.

Comparison of an inflammatory disorder. The method comprises the detection of an interleukh 1 (IL-1) (4411232) haplotype in a sample obtained from the interleukh 1 (IL-1) (4411232) haplotype. The method provides kits for disorder. X16607 to X16631 represent PCR primer used in the method for detecting the IL-1 (44112332) haplotype. The method provides kits for detecting the IL-1 (44112332) haplotype. The method provides kits for detecting the IL-1 (44112332) haplotype. The method provides kits for detecting the IL-1 (44112332) haplotype. The method provides kits for detecting the IL-1 (44112332) haplotype. The method provides kits for detecting the IL-1 (44112332) haplotype. The method provides kits for detecting the IL-1 (44112332) haplotype. The method provides kits for disorders, including coronary artery disease, osteoporosis, nephropathy in diabetes mellitus, alopecia areata, Graves disease, systemic lupus CC envythamatosy ilchem sclerosis and ulcerative colitis. The detection of allowed in fusual dependent diabetes. The identification of a portian disease, and insulficient disease, sociated haplotype enables determination of which alleles from the IL-1 gene cluster are associated with particular CC some alleles from the IL-1 gene cluster are associated with particular CC inflammatory diseases, and insufficient IL-1 production appears to act centrally in the pathology of these diseases. Therefore, the use of IL-1 gene clusters is useful in determining genetic susceptibility to component.
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2-2JWN-1999 (first entry)
Human IL-1ra BAC contiguous DNA sequence 96.
Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition;
                                                                  29-APR-1999 (first entry)
Interleukin 1 (44112332) haplotype PCR primer #10.
Interleukin 1; IL-1; haplotype; inflammatory disorder; alopecia areata; coronary artery disease; osteoporosis; nephropathy; diabetes mellitus; Graves disease; systemic lupus erythamatosus; lichen sclerosis; ulcerative colitis; PCR primer; ss.
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G;
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Camp NJ, Cox A, De Giovine FS, Duff G;
WPI; 99-080814/07.
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X16616 standard; DNA; 20 BP.
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Matches 20; Conservative
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(DGIO/) DE GIOVINE F S.
                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-1998; G01481.
29-MAY-1997; GB-011040.
(CAMP/) CAMP N J.
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
W09854359-A1.
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New isolated nucleic acid encoding the new human cytokine Tango-77 - used to inhibit inflammation and to screen for specific modulators
Frample 5: Figure 4: 226pp: English.

X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences
Containing alternatively spliced forms of human IL-1ra. Such fragments
are used in the method of the invention which describes the isolation of
a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a
conflammation by binding to the interleukin-1 receptor (IL-1R). It may
also bind to a new receptor so could regulate other cellular processes
associated with acute or chronic inflammation, e.g. asthma, chronic
conflammations associated with advaged arthritis, psociasis and inflammatory
Coowel disease. It may also induce or suppress interleukins, cytokines and
growth factors. Modulators of this protein are used to treat or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid encoding the new human cytokine Tango-77 - used to inhibit inflammation and to screen for specific modulators used to inhibit inflammation and to screen for specific modulators X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences containing alternatively spliced forms of human IL-1ra. Such fragments are used in the method of the invention which describes the isolation of a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a member of the cytokine superfamily that is expected to inhibit inflammation by binding to the interleukin-1 receptor (IL-1R). It may also bind to a new receptor so could regulate other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic harman also because it may also as the meaning at the manific processes associated with acute or chronic inflammation, e.g. asthma, chronic harman accordance in architist, psociasis and inflammatory when a new receptor architist, psociasis and inflammatory when a new recent and a manific mani
interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IL-1ra BAC contiguous DNA sequence 41.
Tango-77; human; IL-1ra; cytckine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; regulation; asthma: rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bowel disease. It may also induce or suppress interleukins, cytokines are growth factors. Modulators of this protein are used to treat or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4327 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 1; Length 14690; 100.0%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3299 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3245 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-1998; U16102.
02-UUI-1998; US-091650.
04-AUG-1997; US-054646.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                     (MILL-) MILLENNIUM BIOTHERAPEUTICS INC. Pan Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of IL-1 or its receptor complex. Sequence 14690 BP; 3810 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD 10216 GTTTAGGAATCTTCCCACTT 10235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GTTTAGGAATCTTCCCACTT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                               03-AUG-1998; U16102.
02-JUL-1998; US-091650.
04-AUG-1997; US-054646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 99-153692/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
WO9906426-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simi
Matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X02996;
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21 Simons G. Vos P. Wijbrandi J, Zabeau M;
22 Simons G. Vos P. Wijbrandi J, Zabeau M;
23 Simons G. Vos P. Wijbrandi J, Zabeau M;
24 WPI; 98-159460/14.

DR WPI; 98-159460/14.

DR WPI; 98-159460/14.

PP Transform plants to provide resistance gene - used to PT transform plants to provide resistance to pathogens or pests, PT Transform plants is majors in approximately 9.9 kb sequence located CC around the wild tomato, Lycopersion peruvianum (PI 128657), AFLP CC marker PM14, which comprises the root knot nematode Meloidogyne CC incognita (Mi) resistance gene. The gene can be used to transform CC incognita (Mi) resistance to plant pathogens or pests, particularly nematodes, e.g. root-knot nematodes, or aphids.

CC particularly nematodes, e.g. root-knot nematodes, or aphids.

CC particularly nematodes, e.g. root-knot nematodes, or aphids.
conditions associated with abnormal levels of inflammation, or activity of IL-1 or its receptor complex.
                                                                                                                                                          Gaps
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                                                                                                           Score 20; DB 1; Length .0620; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.0%; Score 16; DB 1; Length 9870; 100.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                     V16457;
07-JUL-1998 (first entry)
Wild tomato Mi resistance gene.
AFLP marker PM14; root knot nematode; Mi; resistance gene; wild tomato; pathogen resistance; pest resistance; aphid; Meloidogyne incognita; ss.
                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                             2411 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3263. 7111
/*taga a
/note- apen reading frame 1"
3491. 7111
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/note= "open reading frame
1936. .3241
                                                                                                                                                        Mismatches
                                        2407 C;
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/note= "AFLP marker PM14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                    its receptor complex.
10620 BP; 2746 A;
                                                                                                                                                      ö
                                                                                                        100.0%;
                                                                                                                                                                                                                   6056 GTTTAGGAATCTTCCCACTT 6075
                                                                                                                                                                                                                                                                                                                                                     V16457 standard; DNA; 9870 BP.
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6921. .7034
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                                                                                                                                                                                               1 GITTAGGAATCTTCCCACTT
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                                                                                                                                                        Conservative
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nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon peruvianum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TTTAGGAATCTTCCCA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
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08-AUG-1997; E04340.
                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                      20;
                                        Sequence
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/note= "Mi gene (copy 1); encodes W55974"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q14631 standard; DNA; 3186 BP
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19-APR-1991; UO2714.
20-APR-1990; US-511715.
(COLD-) COLD SPRING HARBOR.
Wigler MH, COlicelli JJ;
WPI; 91-339841/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 14096 TTTAGGAATCTTCCCA 14111
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/*tag= a
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                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
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                                                                                                                                         US-028191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51952 BP;
                                                                              16-APR-1998.
09-OCT-1997; U18802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                     98-240529/21
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                                                                                                                                            10-OCT-1996;
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                                                                                                                                                                                                                                     Yaghoobi J;
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                FRARE REPRESENTATION OF THE PRESENTATION OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic plants
Claim 1: Fig 5A-D: 48pp; English.
Claim 1: Fig 5A-D: 48pp; English.
This nucleotide sequence comprises the tomato Mi resistance gene
This nucleotide sequence comprises the tomato Mi resistance gene was cloned
che confers resistance against nematodes. It codes for a 1207
amino acid protein (see W27080). The Mi resistance gene was cloned
from a tomato genotype that is resistant to Meloidogyne incognita
check in a markers linked to the Mi resistance gene was cloned
confecular markers linked to the Mi resistance gene; construction of
a high mol.wt. yeast artificial chromosome (YAC) library; physical
mapping of the molecular markers on the YAC clones and YAC contig
configuration of a cosmid library of the YAC clones
harbouring the linked molecular markers; physical fine mapping and
cosmid contig building; genetic characterisation of tomato mutants
cosmid contig building; genetic characterisation of susceptible
plants with the cosmids forming the contig; and complementation
analysis. The invention further relates to genetically transformed
incognital, and to probes and primers useful for identification of
resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Tomato pest resistance Mi gene (copy 1).

Pest resistance; nematode resistance; disease resistance; Mi gene; tomato; transgenic plant; crop protection; biological control; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10071. .14691
/*tag= a
/note= "copy 2 promoter; specifically claimed in
nucleic acid construct of Claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                     Tomato Mi resistance gene.
Mi resistance gene; tomato; nematode resistance;
Meloidogyne incognita; crop protection; transgenic plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tomato Mi resistance gene - for producing nematode-resistant transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 1; Length 9870;
Pred. No. 29;
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/note= "Mi gene (copy 2); encodes W55975"
42798. .44461
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45102. .48944
/*tag= d
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                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-1996; EP-401764.
KEYGE) KEYGENE NV.
Simons G, Vos P, Wijnbrandi J, Zabeau M;
WPI: 98-112270/11.
                                                                                                                                                                                       Lycopersicon esculentum.
Key Location/Oualifiers
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100.0%; Pre
0; }
                                                                                                                                                                                                                                                  3491, .7111
/*tag= a
/note= "Claim 4"
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V13935 standard; DNA; 9870 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16084. .19932
                                                              (first entry)
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TTTAGGAATCTTCCCA 17
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                                                                                                                                                                                                                                                                                                                                             EP-823481-A1.
                                                              20-JUL-1998
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07-JUN-1999
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This is the nucleotide sequence of the tomato Mi locus associated with 1st 1st the nucleotide sequence of the tomatom in this is the nucleotide sequence of the tomatom artificial chomosome (ABC). Mi was localised by genetic analysis to a region of the tomato genome of about 65 kb. DNA corresponding to this sequence analysis of a 52 kb abC3 insert identified 3 open reading frames, one of which is probably a pseudogene. By RNA blot analysis, transcripts of a 52 kb approximately 4 kb corresponding to copy 1 and copy 2 were found in both resistant but not susceptible chamtor cots and in leaves of resistant but not susceptible plants. CDNA sequences corresponding to full-length transcripts of copy 1 (see. V26082) and copy 2 (see V26083) were obtained. The encoded polypeptides (see W55974-75) are 91% identical and contain structural features similar to known leucine-rich repeat (MSS/LRR) family. A recombinant expression cassette comprising an Mi polynucleotide and an operably linked especially tomatoes (claimed). Transgenic plants can also be especially tomatoes (claimed). Transgenic plants can also be constructed usi. 3 a Mi promoter with heterologous genes; the Mi temporal and spatial patterns and at similar levels to resistance temporal canners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                              resistance - useful to produce transgenic plants resistant to these and other pests, and in marker-aided selection to assess cultivars for resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-37N-1992 (lirst entry)
Plasmid pTM72 insert encoding a human cAMP phosphodiesterase.
Cyclic nucleotide; PDE; glioblastoma cell; rollpram-sensitive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complementary screening for genes and prods. - e.g. RAS protein and CAMP, that modify, complement or suppress genetic defect and correct associated phenotypic alteration claim 15; Page 91; 165pp; English.
Plasmid pTM72 contains a human glioblastoma cDNA which encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                       P-PSDB; W55974, W55975.
Nucleic acids encoding Mi polypeptide(s) conferring nematode
resistance - useful to produce transgenic plants resistant to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 16; DB 1; Length 51952; 100.0%; Pred. No. 32; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8647 G;
Bodeau J, Kaloshian I, Milligan S, Williamson VM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8444 C;
                                                                                                                                                                                                                                                  claim 11; Page 24-39; 55pp; English.
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tata_signal
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Plasmid pTM72 (ATCC 68602) insert.
Plasmid pTM72 (ATCC 68602) insert.
Muman; glioblastoma cell; heat shock sensitivity; phosphodiesterase; deficient yeast strain 10DAB; prost, rat DPD phosphodiesterase; pdel-; bovine Ca2+/calmodulin dependent cAMP phosphodiesterase; heart; plasmid; RAS2(val19); pde2-; pTM3; pTM72; pRATDPD; pJC99; rolipram sensitive; ss.
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human low KM, cAMP-specific phospho-di:esterase and nucleic acids encoding it - used to identify binding cpds. useful as encoding it - used to identify binding cpds. useful as therapeutic agents and as probes to evaluate disease states. Claim 3: Page 29-32; 54pp: English.

The cDNA encodes human low Km, cAMP-specific phosphodiesterase, PDE IV(B). The enzyme and fusion proteins can be used to identify ligands and drugs binding to it. These compounds are useful antidepressant, antiasthmatic and antinflammatory agents. Sequence 3890 BP: 1127 A; 846 C; 852 G; 1065 T;
rolipram-sensitive cAMP PDE. The sequence is very closely related to, but distinct from, the rat pRATDPD cDNA insert (see Q1654).

N.B. This sequence is SEQ ID NO. 22 in the specification but is referred to as SEQ ID NO. 23 in the text, 'e.g. on page 32. Sequence 3186 BP; 927 A; 743 C; 734 G; 782 T;
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                                                                                                                                                   Length 3186;
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Brain low Km, cAMP-specific phosphodiesterase cDNA.
Phosphodiesterase; PDE IV(B); brain; ss.
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/product= cAMP phosphodiesterase
                                                                                                                                                     DB 1;
                                                                                                                                                   Score 15.8; D
Pred. No. 35;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
Livi GP, McLaughlin MM, Torphy TJ;
WPI; 94.322667/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
282. .1973
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
139. .2349
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T34375;
                                                                                                                                                                                                                                                                                                                                                                                Q71539 standard; cDNA; 3890 BP
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                                                                                                                                                                                                                                                       79.0%;
89.5%;
                                                                                                                                                                                                                                   2 TTTAGGAATCTTCCCACTT 20
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Best Local Similarity 89.5'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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10-MAR-1994; U02612.
10-MAR-1993; US-029334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-1996.
20-APR-1990; 511715.
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                         RESULT 11
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PT PROBLEM WORDS.

PT AMA MOIS. isolated from human glioblastoma cells - encode

RAS-related or cyclic nucleotide phosphodiesterase proteins

Claim 4: Column 81:88; 101pp; English.

The sequences given in 734374-76 represent plasmid fragments which

CC contain human glioblastoma cell cDNA inserts which are capable of

Correcting the heat shock sensitivity of the phosphodiesterase

CC deficient yeast strain 10DAB. Several cDNA's were isolated and

Sequenced. PTM22 encodes a novel human gene. From computer analysis,

Phosphodiesterase and the rat DPD phosphodiesterase. Sequences related

CC pTM22 were found to be expressed in human heart. Plasmid pTM22 was

CC pTM22 were found to be expressed in human heart. Plasmid pTM22 was

CC to pTM22 were found to be expressed in human heart. Plasmid pTM22 was

CC to pTM22 were found to be expressed in human heart. Plasmid pTM22 was

CC to pTM32 were found to be expressed in human and the pTM32 was

CC trains. It thus appears that the pdel- and pdel- yeast strain 10DAB

CC servation. It he plasmids pTM3 and pTM72 were also characterised. These

CC two different cAMP phosphodiesterase cDMA's were found to be closely

CC pTM3 and pTM2, pC744x and pRATDPD encode rollpram sensitive cAMP

CC phosphodiesterases.

CC pTM3 and pTM2, pC744x and pRATDPD encode rollpram sensitive cAMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Tomato vacuolar invertase gene (genomic).
RNA polymerase II; promoter; cauliflower mosaic virus; CaMV; ss.
Lycopersicon esculentum.
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0
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/note= "sequence matches known plant nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag* g
/note* "sequence matches known plant nuclear
binding sites"
2344. .2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                781 T;
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/note= "sequence matches known plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                734 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.8; DE
Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note* "claim 37, page 80"
3471. 3474
/*tag= d
1846. 1853
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1. .3519
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/note- "claim 35, p
2772. .3519
/*tag- b
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                                LAB.
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2012. .2019
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2178. .2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             927 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.0%;
89.5%;
19-APR-1991; US-688352.
(COLD-) COLD SPRING HARBOR 1
Colicelli JJ, Wigler MH;
WPI; 96-299902/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TTTAGGAATCTTCCCACTT 20
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Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                        P-PSDB; W00093
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465 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%;
85.0%;
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Best Local Similarity 85.0<sup>§</sup>
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                  316. .416
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                                                                                                                                                  /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal sequences.
Sequence 2199 BP;
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21-FEB-1992;
                                                                                                                                                                                                                                                                                  misc_feature
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misc_feature
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Q28507
ID Q28507
AC Q28507;
DT 11-JAN-
DE TOMALO
KW RNA POJ
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Disclosure: Page 64-68; 87pp; English.

In order to increase the soluble solids content of tomato fruit

produced by a tomato plant, a DNA construct contg. DNA encoding an
invertase is introduced. The DNA encoding the invertase is pref.

C operatively linked to a promoter recognised by the plant RNA
popumentally inverted to a promoter recognised by the plant RNA
such as the cauliflower mosaic virus (CaMV) 355 promoter, or a
developmentally regulated promoter that confers fruit specificity
and appropriate temporal control on the expression of the DNA
encoding invertase, e.g. a native Lycopersicon invertase promoter

C or the histidine decarboxylase (HDC) promoter region.

If the DNA encodes an invertase that is not a vacuolar invertase,
DNA encoding invertase is operatively linked to DNA that encodes
c vacuolar targeting sequences, and, if necessary, DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tomato vacuolar invertase gene - useful for producing transgenic plants with higher soluble solid content in fruit, giving greater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-1993 (first entry)
Tomato vacuolar invertase gene (cDNA).
RNA polymerase II; promoter; cauliflower mosaic virus; CaMV; ss.
Lycopersicon esculentum.
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                                                                                                                           binding sites"
2842. .2849
/*tag= k
/note= "sequence matches known plant nuclear binding sites"
3502
                            binding sites"
2510. 2517
/*tag= i
/note= "sequence matches known plant nuclear
 /*tag= h
/note= "sequence matches known plant nuclear
                                                                                                                    /*tag= j
/note= "sequence matches known plant nuclear
                                                                                                                                                                                                                                                                                                                                    22-FEB-1991; US-660344.
04-OCT-1991; US-771331.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
Butler WO, Dickinson CD, Elliott KJ, Fitzmaurice LC;
WPI; 92-316183/38.
                                                                                                                                                                                                                                                /label= franscription_start_site
3520. .7445
/*tag= m
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/*tag= a
/product= vacuolar_invertase
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3619 A;
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                                                                                        binding sites"
2676. .2683
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                                                                                                                                                                                                                                           /*tag= 1
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10798 BP;
                                                                                                                                                                                                                                                                                                                               U01385
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21-FEB-1992; U
                                                                                                                                                                                                                                                                         precursor_rna
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Claim 7; Page 77 + 61-64; B7pp; English.

In order to increase the soluble solids content of tomato fruit produced by a tomato plant, a DNA construct contg. DNA encoding an invertase is introduced. The DNA encoding the invertase is pref. operatively linked to a promoter recognised by the plant RNA operatively linked to a promoter recognised by the plant RNA as the cauliflower mosalc virus (CaNV) 35s promoter, such as the cauliflower mosalc virus (CaNV) 35s promoter, or a developmentally regulated promoter that confers fruit specificity and appropriate temporal control on the expression of the DNA encoding invertase, e.g. a native Lycopersicon invertase promoter. If the DNA encodes an invertase that is not a vacuolar invertase, DNA encoding invertase is operatively linked to DNA that encodes is and invertase is operatively linked to DNA that encodes is and invertase is operatively linked to DNA that encodes is and invertase is operatively linked to DNA that encodes is and invertase is operatively linked to DNA that encodes is and in the DNA encoding invertase is operatively linked to DNA that encodes is and invertase is operatively linked to DNA that encodes is and invertance in the contains invertase.
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/*tag- c
/label= C-terminal_propeptide
/note= a sequence effective for vacuolar targeting
comprises at least this sequence"
1798. 1914
                                                                                                                                                                                                                                                                                                                                                                              /label- active_site
/note= "this region appears to be the active site
of invertase, partic. nucleotides 898. .924"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tomato vacuolar invertase gene - useful for producing transgenic plants with higher soluble solid content in fruit, giving greater commercial value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= h
/note= ""active site" probes may be derived from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= active_site
/note= "region 889. .927 appears to be the ad
of invertase, partic nucleotides 898. .924"
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11-JAN-1993 (first entry)
Tomato vacuolar invertase gene (genomic).
RNA polymerase II; promoter; histidine decarboxylase; HDC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-1991; US-660344.
04-COT-1991; US-77331.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
BUTLER WO, DICKINSON CD, Elliott KJ, Fitzmaurice LC;
WROND Y, Mirkov TE;
WPI: 92-316188/78.
P-PSDB; R27007.
                                                                                                                                                                                                  Score 15.2; DE
Pred. No. 68;
0; Mismatches
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Trit, 2. JULY 1970.

Tomato vacuolar invertase gene - useful for producing transgenic plants with higher soluble solid content in fruit, giving greater commercial value and content in fruit, giving greater Disclosure; Page 71-75; 87pp; English.

Disclosure; Page 71-75; 87pp; English.

In order to increase the soluble solids content of tomato fruit produced by a tomato plant, a DNA construct contg. DNA encoding an invertase is introduced. The DNA encoding the invertase is pref. Copymerase II. The promoter recognised by the plant RNA polymerase II. The promoter recognised by the plant RNA polymerase II. The promoter recognised by the plant RNA colymerase II. The promoter recognised by the plant RNA polymerase II. The promoter recognised by the plant RNA colymerase II. The promoter mast be a constitutive promoter, and appropriate temporal control on the expression of the DNA encoding invertase, e.g. a native Lycopersicon invertase promoter if the DNA encoding invertase, is operatively linked to DNA that encodes invertase, common or control of the cessary, DNA encoding signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3770 T;
                                                     /*tag- a
//*tag- a
//*tag- a
//note= "claim 34, page 80"
3637. 3640
3640. 1853
/*tag- c
//note= 'sequence matches known plant nuclear
                                                                                                                                                                                                                                               /*tag- e //rag- e //rag- e //rag- sequence matches known plant nuclear binding sites. 2510. 2517 /*tag- f //rag- f //rag- f //rag- sequence matches known plant nuclear binding sites. 2676. 2683
                                                                                                                                                           binding sites"
2178 - 2185
7-tag - d
/note= "sequence matches known plant nuclear
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/note= "sequence matches known plant nuclear
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2842. .2849
7-tag= "equence matches known plant nuclear
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binding sites"
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04-OCT-1991; US-771331.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
BULLER WO, Dickinson CD, Elliott KJ, Fitzmaurice LC; Konno Y, Mirkoy TE; WPI; 92-316183/38.
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/label= transcription_start_site
3686. .7612
/*tag= k
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                       Location/Qualifiers
1. .3679
cauliflower mosaic virus; CaMV; ss. Lycopersicon pimpinellifolium.
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2344. .2351
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3008. .3015
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Sequence
                                                                                    tata_signal
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                                              promoter
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Score 15.2; DB 1; Length 10965; Pred. No. 73;

76.0%; 85.0%;

Query Match Best Local Similarity

Search completed: September 18, 1999, 05:27:20 Job time: 1685 sec

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September 18, 1999, 06:47:34; Search time 1405 Seconds (without alignments) 28.079 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                         2546578 segs, 986266752 residues
                              · nucleic search, using sw model
                                                                                         GTTTAGGAATCTTCCCACTT 20
                                                                         US-09-037-472-4
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1 GTTTAGGAATCTTCC
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em_est5:*
em_est6:*
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gb_est6:*
gb_est18:*
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em_est21:
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Perfect score:
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H26538 y113906.rl
H67402 yu55h06.sl
N87127 L2378F Huma
H09278 y198f10.rl
R41046 HK464-f Adu
H56501 yt88a03.rl
H6755 yu52q08.rl
M79435 zd78p03.rl
AA431115 zw69f10.r
C48917 c48917 yujj
C50747 C50747 Yujj
C50747 C50747 Yujj
C50747 C50747 Yujj
AA781119 aj23f08.s
AA98880 0099f01.s
AA98880 0099f01.s
AA98180 gq99f01.s
H6718 yu66f03.rl
H6718 yu66f03.rl
H6718 yu66f03.rl
H65209 yu66f03.rl
H6718 Yu66f03.rl
H7888 10169 Lambd
D15818 R1CC137A R
H3778 yy56f05.rl
W33002 yz88f01.rl
W33002 yz88f01.rl
                                                                                                                                                                                                                                  AA290364 vb39a03.r
AA307102 EST178016
AA31000 EST181467
AA651990 ns49e02.s
AA651910 vt14h04.r
AA71473 vu26b05.r
AA77446 oa49a05.s
AA737486 oa49a05.s
                                                                                                                                                                                                                                                                      F22980 SSC17H07 PO AA989956 ua55a04.r Al044527 Homo sapi
                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                    12-JUL-1995
                                                             Description
                                                                                                                                                                                                                                                                                                    yll3g06.rl Soares breast 2NbHBst Homo sapiens cDNA clone HMAGE:158170 5', mRNA sequence. 4896528 H26538.1 GI:ROFFT
                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                               SUMMARIES
                                                                                                                                                                               AA692500
AA960919
AV047898
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AA988380
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AA307102
AA310600
AA651989
AA691910
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R41046
R47346
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H64718
H65209
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H67402
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T49306
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W79493
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C50747
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Treyaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                         Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
Insert Size: 911
High quality sequence stops: 282
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 911 Std Error: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 282.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N87127 298 bp mRNA EST 01-APR-1996
L2378F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA
clone L2378 5' similar to REPETITIVE ELEMENT ALU, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 298)
                                                                                                                                                                                97044478
On Jan 24, 1995 this sequence version replaced gi:634117
                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:229787"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 100.0%; P. 16; Conservative 0;
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                                                                                                                          and Marra, M.
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Best Local Similarity
Matches 16; Conserv
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JOURNAL
MEDLINE
COMMENT
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stops: 203
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: MI3RPl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 395)
                                                               Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Homo.
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 363)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holhman,M., Hultman,M., Kucaba,T., Le,M., Lenon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.4; DB 23; Length 362;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares breast 2NbHBst"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:572071"
/db_xref="taxon:9606"
/clone="IMAGE:158170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 203.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 9
                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                    The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230. Library
Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.0%;
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H67402.1 GI:1026142
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                                                                                                                                                                                                                                                                                    Contact: Wilson RK
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                                                   Homo sapiens
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Best Local
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DEFINITION
                                                 ORGANISM
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JOURNAL
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          KEYWORDS
SOURCE
                                                                                                        REFERENCE
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H67402
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Gaps

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High qality sequence stops: 247 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE consortium (info@image.llnl.gov) for further information. Insert Length: 374 Std Error: 0.00 Seq primer: M13RPl Sequence stop: 247.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1282 Std Error: 0.00 seq primer: MI3R21 High quality sequence stop: 383.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    нуэг/8 480 bp mRNA EST 23-JUN-1995
y198f10.r1 Soares infant brain INIB Homo sapiens cDNA clone
H09278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
1 Hillar, L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevarskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU Merck EST Project
Unpublished (1995)
On May 5, 1995 this sequence version replaced gi:798447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8; DB 20; Length 353;
Pred. No. 2.3e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 TTTAGGAGTCTTCCCATT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
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H09278.1 GI:874100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson, R.
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KEYWORDS
SOURCE
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Ya74b08.rl Stratagene placenta (#937225) Homo sapiens cDNA clone
IMAGE:67383 5' similar to similar to gb:L06132 OUTER MITOCHONDRIAL
MEMBRANE PROTEIN PORIN (HUMAN), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primaces; Catarrhini; Hominidae; Homo.

1 (bases 1 to 353)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Ghissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,

Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,

Mardis,E., Moores,B., Moorris,M., Parsonos,J., Prange,C., Rifkin,L.,

Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,

Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                         Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tal: 4169788558
Email: liewcc@utcc.utoronto.ca
Seq primer: GAAATTAAACCTGACTAAAAGGG.
   Liew,C.C.
CDNAs from fetal heart (1996)
Unpublished (1996)
On May 5, 1995 this sequence version replaced gi:798440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Sep 21, 1992 this sequence version replaced gi:278958.
Other_ESTs: ya74b08.s1
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.0%; Score 16; DB
100.0%; Pred. No. 1.9
ive 0; Mismatches
                                                                                                                                                                                                                                                                1. .298
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21"
                                                                                                                                                                                                                                               Location/Qualifiers
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T49306.1 GI:651166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 AGGAATCTTCCCACTT 93
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SOURCE
ORGANISM
AUTHORS
TITLE
JOURNAL
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DEFINITION
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JOURNAL
MEDLINE
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T49306
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Gaps

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/map="21"

/clone='e814-r"

/clone_lib="&e14 rult heart, Clontech"

/lab_host="E. coli Y1090"

/note="Vector: Lambda gtll; Site_l: EcoRI; Site_2: EcoRI"

/note="Vector: Q2 g 101 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Waye Mary M.Y.
Department of Biochemistry
The Chinese University of Hong Kong
Tha 302C, Basic Medical Science Building, The Chinese University of
Hong Kong, Shatin, N.T., Hong Kong.
                                                                                                                                                                                                                                                                 R47346 360 bp mRNA EST 16-MAY-1995
He814-r Adult heart, Clontech Homo sapiens cDNA clone e814-r, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotzi Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases I to 360)

Waye, M. M. Y., Cheung, H. K. Y., Lam, W. Y., Law, P. T. W., Lo, A. S. Y., Lui, V. W. Y., Luk, S. C. W., Tsui, S. K. W., Tung, C. K. C., Yam, N. Y. H., Inew, C. C. and Lee, C. Y.

Gene expression of adult human heart as revealed by random sequencing of const library
Miami Winter BioTechnol. Symp. Proc. 6, 90 (1995)
                                                                                       Gaps
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IMAGE:231340 5', mRNA sequence.
91005145
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                                                  Length 271;
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                                                                                       Indels
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Pred. No. 2.3e+02;
0; Mismatches 2;
                                              Query Match 79.0%; Score 15.8; DB 22; Best Local Similarity 89.5%; Pred. No. 2.3e+02; Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: D133723@vax.csc.cuhk.hk
Insert Length: 927 Std Error: 0.00
Seq primer: GGTGGGGGGACTCCTGGAGCC
High quality sequence stop: 201.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21"
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89.5%;
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                                                                                                                             2 TITAGGAATCTTCCCACTT 20
                                                                                                                                                                                                                                                                                                                                                              R47346.1 GI:808217
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Best Local Similarity 89.5'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 8526035123
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                       sequence.
                                                                                                                                                                                                                                                                                                                                                                                                      human.
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ORIGIN
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NID
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AUTHORS
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R47346/c
                                                                                                                                                                                                                                                                                                                       ACCESSION
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KEYWORDS
SOURCE
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H56501
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                                                                                                                         Contact: Waye Mary M.Y.

Department of Biochemistry
The Chinese University of Hong
The Station, N.T., Hong Kong.
Hong Kong, Shatin, N.T., Hong Kong.
Theil 8526096874
Fax: 8526038123
Email: b1337230vax.csc.cuhk.hk
Tinsert Length: 1795 Std Error: 0.00
Seq primer: GGTGGCGACGACTCCTGGAGCC
High quality sequence stop: 277.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Adult heart, Clontech"
/lab_host="E. coli Y1090"
/note="Vector: Lambda gill; Site_l: EcoRI; Site_2: EcoRI"
/l c 49 g 59 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R41046 271 bp mRNA EST 16-MAY-1995
Hk464-f Adult heart, Clontech Homo sapiens cDNA clone k464-f, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 271)

Maye, M. M. Y., Cheung, H. K. Y., Lam, W. Y., Law, P. T. W., Lo, A. S. Y.,

Liu, V. W. Y., Luk, S. C. W., Tsui, S. K. W., Tung, C. K. C., Yam, N. Y. H.,

Gene expression of adult human heart as revealed by random

Sequencing of CDNA library

Minami Winter BioTechnol. Symp. Proc. 6, 90 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 22; Length 480;
Pred. No. 2.3e+02;
0; Mismatches 2; Indels 0
                                                                                           /clone_lib="Soares infant brain lNIB"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="X"
/organism="Homo sapiens"
                                /db_xref="taxon:9606"
                /db_xref-"GDB:418856
                                                                        /clone-"IMAGE:46315"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="k464-f"
                                                                                                                                                                                                                                                                                                                                                                                                                    79.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9798662
R41046.1 GI:798662
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.0
Best Local Similarity 89.5
Matches 17; Conservative
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R41046/c
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ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE COMMENT

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1. 559
/Organism="Homo sapiens"
//db_xref="Color=3780886"
//db_xref="Color=3780886"
//db_xref="Color=3780886"
//db_xref="Color=388086"
//clone="IMAGE:229790"
//clone="IMAGE:229790"
//clone="IMAGE:229790"
//clone="IMAGE:229790"
//dev_stage="20 week-post conception fetus"
//dev_stage="20 week-post conception fetus"
//lab_host="DH108 (ampicillin resistant)"
//lab_host="DH108 (ampicillin resistant)"
//lab_host="DH108 (ampicillin resistant)"
//dev_stage="20 week-post conception fetus"
//dev_stage="20 week-post conception fetus"
//dev_stage="20 yellow and spleen; Vetoci: pT730 (Pharmacia)
//dev_stage="20 yellow and lighted to Eco RI adaptors
//double-stranded cDNA was lighted to Eco RI adaptors
//dev_stage="20 yellow and lighted pT773 vector: Library
//dev_stage="20 yellow and proper yellow and Eco RI adaptors
//dev_stage="20 yellow and of normalization: Library
//dev_stage="20 yellow and proper yellow and yellow and
                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 559)

1 Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, M., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                     Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: estewatson.wustl.edu
Insert Size: 1381
High quality sequence stops: 331
Source: IMAGE Consortium, LLNL
IMAGE Consortium (info@inage.llnl.gov) for further information.
Seq. primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W79493 433 bp mRNA EST 17-OCT-1996 zd78h03.rl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346805 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Jan 24, 1995 this sequence version replaced gi:634184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 559;
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4444 Forest Park Parkway, Box 8501, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 331.
Location/Qualifiers
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W79493.1 GI:1390753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
      Homo sapiens
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                                                                                             REFERENCE
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W79493
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Butkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 463)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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Yu52908.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:229790 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Size: 833
High quality sequence stops: 349
Source: IMAGE Consortium Linl.
This clone is available royalty free through Linl.; contact the INAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 83 Std Brror: 0.00
Seq primer: MI3RPL
High quality sequence stop: 349.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On May 8, 1995 this sequence version replaced gi:801436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"/db_xref="GDB:3861331"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 TITGGGAATCTICCCCCTT 414
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91026195
H67455.1
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FEATURES

BASE COUNT ORIGIN

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ACCESSION

VERSION KEYWORDS SOURCE

RESULT H67455/c

g

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Gaps

us-09-037-472-4.rst

TITLE JOURNAL

COMMENT

FEATURES

REFERENCE AUTHORS

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="lib" Soares_testis_NHT"
/sex="male"
/lab_host="PH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylainker; Site=1: Not I; Site=2: Eco RI: 1st strand cDNA
was prepared from mRNA obtained from Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 127 c 81 g 149 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C45344 11 10-SEP-1997 C45344 Yuji Kobara unpublished cDNA Caenorhabditis elegans cDNA clone yk393c1 5', mRNA sequence.
                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 451.
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Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Unpublished (1996)
White,Y., Wylie,T., Waterston,R. and Wilson,R. wash-Werck EST Project 1997. Unpublished (1997) on Sep 12, 1996 this sequence version replaced gi:1407164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On May 9, 1995 this sequence version replaced gi:802599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.0%; Score 15.8; DB 33; Length 458; Best Local Similarity 89.5%; Pred. No. 2.3e+02; Matches 17; Conservative 0; Mismatches 2; Indels 0;
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Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 0559-75-0771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g2381597
C45344.1 GI:2381597
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                                                                                                                         Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                      .458
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2w69f10.rl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781483
5', mRNA sequence.
AA431115
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 458)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1809 Std Error: 0.00
Seq primer: mob.REGA+ET.
Location/Qualifiers
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       Chordata; Craniata; Vertebrata; Mammalia;
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rikfin,L., Rohlfing,T., Soares,M., Tan,F.,
Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Soares_fetal_heart_NbHH19W"
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/db_xref="taxon:9606"
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                                                                                                                                                                                             The WashU-Merck EST Project
Unpublished (1995)
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BASE COUNT ORIGIN

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AA431115

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ORGANISM

KEYWORDS SOURCE

VERSION

REFERENCE

AUTHORS

Gaps

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us-09-037-472-4.rst

FEATURES

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Eukaryotta; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditida; Rhabditina; Rhabditida; Rhabditida; I (bases 1 to 380)

Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A. and Nishigaki,A.

Expression map of the C.elegans genome
Unpublished (1996)
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AA781119
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                C50747 380 bp mRNA EST 11-SEP-1997 (S50747 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk524g1 5', mRNA sequence.
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Email: 1031,496-1550
Email: Robert Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1400787.
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On Sep 12, 1996 this sequence version replaced gi:1394369.
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/note="dev_stage="varied"
/iote="dev_stage="varied"
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Pred. No. 2.3e+02;
0; Mismatches 2;
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
TT: 0559-75-0771
Fax: 0559-75-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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89.5%;
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 0559-75-0771
Fax: 0559-75-6240
Email: ykoharadddbj.nig.ac.j.
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Pred. No. 2.3e+02;
0; Mismatches 2;
        Email: ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

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BASE COUNT ORIGIN

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FEATURES

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Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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79.0%; Score 15.8; DB 38; Length 440; 89.5%; Pred. No. 2.3e+02; Live 0; Mismatches 2; Indels 0

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X04500 Human gene
AL024497 Human DNA
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L19314 Human HRY g
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AC005712 Homo sapi
AC00772 Homo sapi
AC017013 Escherichia
AR02203 E.coli rpiR
AE000482 Escherichia
AE000482 Escherichia
AE000482 Escherichia

Title: Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Searched: Database

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DB 5;
0.49;
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Kornman, K. S. and Duff, G.W.
Detecting genetic predisposition to
Patent: US 5686246-A 3 11-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3 from patent US 5686246. 173227 93009366 I7327.1 GI:3007.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                           HUAC002544
HUU91326
                                                                                                                                                 MLCB33
AB001479
AC006267
AF099081
AF007720
AC007012
AR012073
AR025198
DDPTATPAS
                                                                                                                                                                                                                                                                                                                                                                                                                           MMHC214016
MMHC322F16
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No.
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RATHAIRY
RATHES1A
AB012572
AC006468
  HSILIB
HS283K11
XLU36194
HUMHAIRY
HSPC13M
AE000841
GOGDH
ATY12227
AC007067
T22318
HSU46025
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HS134E15
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ECRPIRB
AE000482
AF109904
ATFCA2
SCPBR1
AC03970
AF003970
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4 c 5 g
  100.0%;
100.0%;
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92.0 140682
87.0 15069
87.0 15069
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87.0 15069
84.0 10051
84.0 12898
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Unclassified.
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ORIGIN
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TITLE
JOURNAL
FEATURES
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KEYWORDS
SOURCE
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  RESULT
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                                                                         0; Search time 436.05 Seconds
(without alignments)
145.869 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
       GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                     679419 seqs, 1590154680 residues
                                                                        September 18, 1999, 15:48:40
                                                  nucleic search, using sw model
                                                                                                                    US-09-037-472-3
20
1 TGGCATTGATCTGGTTCATC
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1: 9b_bal:*

3: 9b_bal:*

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7: 9b_pli:*

10: 9b_pli:*

10: 9b_pri:*

11: 9b_rr:*

11: 9b_rr:*

11: 9b_rr:*

12: 9b_rr:*

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gb_htg1:*
gb_htg2:*
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em_hum4:*
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em_ph:*
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297337 Arabidopsis 246262 S.cerevisia AC003970 Arabidops AF025410 Rhodospor AF104107 Triticum 019028 Saccharcmyc AP00019 Homo sapi AL022067 Human DNA AF111102 Mus muscu AF111103 Muse mscu AF111103 Muse mscu AF111103 Muse helix 104527 Rattus norv D13417 Rat mRNA fo AB012572 Gallid he AB012572 Gallid he AB012572 Gallid he

23-DEC-1997

PAT

periodontal disease

Length 20;

5;

Score

Result No.

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HS283K11 140682 bp DNA PRI 23-APR-1999
Human DNA sequence from clone 283K11 on chromosome 6q23.1-24.3.
Contains part of the EYA4 gene for eyes absent (Drosophila) homolog
A. Contains ESTs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7419. .7426
/note="pot. viral enhancer core sequence"
8127. .8953
                                                                                                                                                    4274. .4279
/note="pot.viral enhancer core sequence"
/note="alu repeat"
/note="alu repeat"
5125. .5326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(6916. .6924)

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complement(7247. .753)

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      /note="pot.viral enhancer core sequence"
2858. .2865
                    2858. .2865
/note-"pot.viral enhancer core sequence"
3092. .3143
                                                                                                                        /note="pot.viral enhancer core sequence" 4274. .4279
                                                                                                                                                                                                                                                                           5489...5497
/note-"pot.viral enhancer core sequence"
5874...6038
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/note="pot.viral enhancer core sequence"
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100.0%; Pred. No. 1.7;
tive 0; Mismatches 0;
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/note="inverted repeat A'"
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6213. .6220
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8953
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1 2328 c 2122 g
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HTG; EYA4; eyes absent.
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                                                                                      .5124
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6039. .727
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5489. .549
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KEYWORDS
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HS283K11
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DGGIOLRISSHHYSKGFRQAASVVVAMDKLBKMLYPCPQTFQENDLSFFFFIFEEF
DGGIOLRISSHHYSKGFRQAASVVVAMDKLBKMLYPCPQTFQENDLSFFFFIFEEF
FFDTWDNEAYVHDAPVRSLNCTLRDSQKSLWANSGPYELKALHLQGQDWDEQQVVFSM
FRIEINNKLEFESAQFPWYISTSQAENWPVFLGGTKGGQDITDFTWQFVSS"
// Number=2
complement(2714..2721)
 ö
                                                                                                                                                                                                                                                                                                                                                                                                          Erratum:[[published erratum appears in Nucleic Acids Res 1987 Jan
26;15(2):868]]
                                                                                                                                                                                                                                                                           Eukaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates: Catarrhini; Hominidae; Homo. 1 (bases 1 to 9721) [1 (bases 1 to 9721)] [1 (candy, M. S., Webb, A.C. and Auron, P.E. Genomic sequence for human prointerleukin 1 beta: possible volution from a reverse transcribed prointerleukin 1 alpha gene 87040762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'number-2
join(2481. .2527,3092. .3143,5125. .5326,5874. .6038,
7275. .7405,8127. .8339)
   Gaps
                                                                                                                                                    26-JUN-1997
 0;
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2006. .2465
/number=1
2039. .2055
/note="direct repeat 2"
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Thote="pot. viral enhancer core sequence"

2458. 2455

Thote="pot. viral enhancer core sequence"

2466. 2527
   Indels
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1. .9721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"

/db_xref="taxon:9606"

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/clone_lib="leukocyte DNA library"

/map="q13-q24"

/669. 960

/note="Alu repeat"

1576. 1581

/note="TATA-box like sequence"

1809. 1816
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/db_xref="SWISS-PROT:P01584"
                                                                                                                                      HSILIB 9721 bp DNA
Human gene for prointerleukin 1 beta.
X04500
 Mismatches
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1934. .8953
1934. .2005
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AUTHORS
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Gaps

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Length 9721;

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              Bray-Allen,S.

Direct Submission

La Submitted (16-APR-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Apr 25, 1999 this sequence version replaced gi:4581315.
During sequence assembly data is comparated from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence is the entire insert of clone 283K11. This sequence
has been finished according to sequencing problems, such as
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 283K11 is from the library RPCII constructed at the Roswell Park Cancer Institute by the group of pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECIOR: pcrPAC2.
                                                                                                                                                                                                                                                                                                                                                                                annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7320. .7617 .
/note="AluSx repeat: matches 2. .299 of consensus"
7518. .7768
/note="L1MA3 repeat: matches 5102. .6252 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="3 copies 40 mer 78% conserved"
267. 7319
note="LiMA3 repeat: matches 6252. .6304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6929. .7114
/note="L2 repeat: matches 2054. .2276 of consensus"
7117. .7262
/note="73 copies 2 mer ta 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5871. .5980
/note="MIR repeat: matches 77. .204 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        515. .560
/note="23 copies 2 mer ag 96% conserved"
517. .560
/note="11 copies 4 mer agag 98% conserved"
704. .751
/note="MIR repeat: matches 21. .70 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .247 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1119. .7262
note="36 copies 4 mer tata 75% conserved"
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/note="MER5A repeat: matches 9.
complement(2631. .3056)
/note="match: GSS AQ038582"
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'note="MER5A repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4154. .4373
/note="MIR_repeat: matches 10.
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/map="q23.1-24.3"
/clone_lib="RPC11"
  (bases 1 to 140682)
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/note="3 coni
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AUTHORS
                                          TITLE
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complement(join(<19490. .19573,21006. .21142,33874. .34039,37747. .37826,39841. .39984,40128. .40270,41425. .41491,45957. .46049,54426. .54494,55851. .55975,120164. .>120213))
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AD_XTEET="FID: G4680188"

AD_XTEET="G1: 4680188"

AD
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product="dJ283K11." (eyes absent (Drosophila) homolog 4)"
/protein_id="CAB41291."
/db_xref="PID:e1426176"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mote="match: proteins 099504 P97767 099502 008575 000167 060647 P97480; match: cDMSA X17114 U81602 U81604 U61112 AF031484 X17115 U71208 U81603 U61111 AJ000098 AJ000097 U61110; match: ESTS AA176744 A1426738"
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// note="L2 repeat: matches 872. .1276 of consensus"
21788. .22161
// note="MERS3 repeat: matches 5. .323 of consensus"
22162. .22681
// note="L2 repeat: matches 1276. .1796 of consensus"
24053. .24372
// note="L1ME1 repeat: matches 5569. .5894 of consensus"
// note="L1ME1 repeat: matches 5569. .5560 of consensus"
// note="L1ME1 repeat: matches 5270. .5560 of consensus"
// note="24739. .24739"
// note="26 copies 2 mer tg 75% conserved"
                                                                                                                          /note="L1MA3 repeat: matches 3510. .6102 of consensus" 10634. .10935
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25398. .25769

7.00ce="THBIC repeat: matches 1. .367 of consensus"
25770. .26468 repeat: matches 5556. .6270 of consensus"
26470. .26553

7.00ce="FRAM/FAM repeat: matches 5. .88 of consensus"
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/note="Alujb repeat: matches 3. .268 of consensus"
8047. .10633
                                                                                                                                                                                                                             .301 of consensus"
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/note="MIR repeat: matches 3. .192 of consensus"
25038. .25397
                                                                                                                                                                                                                    /note="AluY repeat: matches 1.
10936. .15783
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/gene="EYA4"
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                                                                                                                                                                                                                                                                                                                                                                                                                              //unction="helix-loop-helix transcription factor"
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Turner, D.L.

Direct Submission
Submitted (12-SEP-1995) David L. Turner, Genetics, Fred Hutchinson
Cancer Research Center, 1124 Columbia St., A3-025, Seattle, WA
98104, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(1707. .1814,1943. .2038,2287. .2373,3006. .3557)
/gene="HRV"
join(1707. .1814,1943. .2038,2287. .2373.3006
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/gene="HRY"
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                                                                                                                                                                                                                                                     /organism="Xenopus laevis"
/db_xref="taxon:8355"
27. .827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.4; 1
Pred. No. 28;
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94.7%;
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Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                               / Anote="MER96 repeat: matches 3. .175 of consensus" / Anote="Lize repeat: matches 2671. .2743 of consensus" 29272. .29343 // Anote="Lize repeat: matches 2671. .2743 of consensus" 29536. .29637. .29637. .29636. .32712 // Anote="Lime1 repeat: matches 5195. .5300 of consensus" 27055. .33714 // Anote="Lime1 repeat: matches 2276. .5351 of consensus" 23705. .33374 // Anote="Lize repeat: matches 23. .257 of consensus" 25473. .36374 // Anote="Lize repeat: matches 1969. .2693 of consensus" 26469. .36048 // Anote="Lize repeat: matches 1969. .2693 of consensus" 26469. .36048 // Anote="Lize repeat: matches 2571. .2710 of consensus" // Anote="Lize repeat: matches 2571. .2710 of consensus" // Anote="Lize repeat: matches 2571. .2710 of consensus" // Anotes="Lize repeat: matches" // Anotes="Lize repeat: matches 2571. .2710 of consensus" // Anotes 2571. .2710 of consensus // Anotes 2571. .2710 of c
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Xenopus laevis helix-loop-helix transcription factor hairyl mRNA,
complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
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Dawson,S.R., Turner,D.L., Weintraub,H. and Parkhurst,S.M.
Specificity for the Hairy/Enhancer of split bHiH proteins maps outside the bHiH domain, and suggests two separable modes of transcriptional repression
Mol. Cell. Biol. (1995) In press
2 (bases 1 to 1069)
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47957. .48165
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/note="MIR repeat: matches 8. .237 of consensus"
49367. .49695
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37592. .38335
/gene="EYA4"
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                                                                                    /note="match: GSS AQ356291"
28709. .28826
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Pred. No. 21;
    complement(27606. .27958)
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/strain="delta
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162. .2117
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                                                                                  1 TGGCATTGATCTGGTTCAT 19
                                               Conservative
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       Query Match
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Matches 18; Conserv
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VVITYLDDGLEWNHTDIYANYDPEASYDFNDNDHDPFPRYDPTNENKHGTRCAGEIAM
OWNHKGCGVOVAYNSKYGGIRNLDGIYTDAIEBASIGFNDFGHYDIYSASNGFNDDGKY
VEGFORLAOKARFYVKOGRGIRYLDGITYDAIEBASIGFNDFGHYDIYSASNGFNDDGKY
VEGFORLAOKARFYVKOGRGIRYLTSAGNGGROGDNCDCDGYTDSITISISSA
SQQGLSPWYAEKCSSTLATSYSGGDYTDORTISADLHNCTFTHTGTSASAPLAAGIF
ALALEANPNLTWRDMQHLVVWTSEYDDLANNPGWKKNGAGLMVNSRFGFGLLNAKALV
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Aasalaeelgydllggigslenhylfkhknhprrsrrsafhitkrlsdddrviwaeqo
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FEATIEYSRRGDLHVTLISAAGTSTVLLAERERDISPNGFKNWDFMSVHTWGENPIGT
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QSPKKSPSAKLNIPYENFYEALEKLNKPSQLKDSEDSLYNDYVDVFYNTKPYKHRDDR
LLQALVDILNEEN"
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Creemers, J.W., Roebroek, A.J. and Van de Ven, W.J.
Creemers, J.W., Boebroek, A.J. and Van de Ven, W.J.
Expression in human lung tumor cells of the proprotein processing enzyme PCI/PC3. Cloning and primary sequence of a 5 kb cDNA
FEBS Lett. 300 (1), 82-88 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (12-JUN-1992) A.J.M. Roebroek, Universitaire
Ziekenhuizen, Leuven, Centrum voor Menselijke Erfelijkheid, UZ
Gasthuisberg, Herestraat 49 3000 Leuven, BELGIUM
Location/Qualifiers
1. .5037
                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                             Homo Sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="human lung cancer: carcinoid tumor"
1. .189
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                                                                            DB 9; Length 5552;
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/function="proprotein processing enzyme"
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/protein_id="CAA46031.1"
/db_xref="PID:q35318"
/db_xref="G1:35318"
/db_xref="G1:35318"
                                                                        Score 17.4; DE
Pred. No. 39;
0; Mismatches
 1272
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/db_xref="taxon:9606"
   φ
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H.sapiens encoding PC1/PC3.
K4810 S88573
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X64810.1 GI:35317
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                                                                        Query Match
Best Local Similarity 94.7
Matches 18; Conservative
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/taanslation-Wakvettroaleyangpthlghlrstytpadiyaryrrlrgddvl
FVOATDEHCTPIAVKAEAEGRTPLEVATRYHEMIRGDLERCDISFDSFTRTTDELHHE
IAQWFEKLKIVERGFTYEKDIRGLYCGCOGRFTPLDRYVBGTCEYCGSGGARGDHCEGCG
RHLEPLQLEDPRCHVCGSEPEVRDSRHYFRELNGFODEIREWIEGSENBNURNYAIO
WLREGLKDWILTRDMEWGVQVPLEGNEGKIIYVWGEARLGYISSAAAWSKKTGRDWRE
YWDSGATHFIGGNIIYHALFWPALLMAYGGRTPANIIAGFVLLEGQKMSTSKNWVV
WTSDFLERPDRLLRYYLTVNAPLTRDTDFSWDDFORWVDELADVLGNELARFRESFT
GRFPDGRVPAAGELTARDLERLESIRAAHDTVAELLDKFOFRDALMHIKLARRGNKY
FNDOEPWRAVKESPARSTCLHLCNLLAANLGKLLKFOFRDALMHIKLARRGNKY
FHELREGOVIERARPLFSKITDEANLGKLLRFPMSAAGRILSIMNLEDEAWG
FHELREGOVIERARPLESIRGAAIEEEKAKLIEEDDEVETVTIDDFTTMDIRVGVIR
SAGNLLATGESLNILDPGDAENGERIR"
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Smith, D.R.
Direct Submission
Submitted (10.AUG-1997) Genomics and Technology Development, Genome Therapuetics Corporation, 100 Beaver Street, Waltham, MA
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Appene—WHTH87"

/note—"Function Code:10.07 - Metabolism of Macromolecules,

Aminoacyl tRNA synthetases and tRNA modification ; similar

/codon_start=11

/transl_table=11
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Smith, D.R., Doucette-Stamm, L.A., Deloughery, C., Lee, H.-M.,
Dubois, J., Aldredge, T., Bashirzadeh, R., Blakely, D., Cook, R.,
Gilbert, K., Harrison, D., Hoang, L., Keagle, P., Lumm, W., Pothier, B.
Qiu, D., Spadafora, R., Vicare, R., Wang, Y., Wierzbowski, J.,
Gibson, R., Jiwani, N., Caruso, A., Bush, D., Safer, H., Patwell, D.,
Prabhakar, S., McDougall, S., Shimer, G., Goyal, A., Pietrovski, S.,
Church, G.M., Daniels, C.J., Mao, J.-i., Rice, P., Nolling, J. and
                                                                                                                                                                                                                                                                                                                                                                  AE000841 10051 bp DNA BCT 16-APR-1998 Methanobacterium thermoautotrophicum from bases 525786 to 535836 (section 47 of 148) of the complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanobacterium thermoautotrophicum.
Methanobacterium thermoautotrophicum
Archaea: Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
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    10051
/organism="Methanobacterium thermoautotrophicum"

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       Length 5037;
                                                                          Indels
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/db_xref="PID:92621666"
/db_xref="GI:2621666"
                                                                      1;
   DB 10;
Score 17.4; DE Pred. No. 38; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:2166"
/clone="MTH"
162. .2117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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CDS

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/product="conserved protein"
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AYIMRIKEAGGTAVVTYTEGSADPKVETMLKAVVDNIIHLDGSELTVEAMVGIGRVSA
PYTIDDSGIRKVVHEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSENYSTGIAGLDAVLGKPEFGYLMLLTGPPKVGKTVLATEFTY
ALGRRNPCLEIAARYGYRDGNNTHAFNWFTGSLADKLHYTDLPTGLAGGRPBDSGN
VRYSAIONTTDLMYKVGISTRSLYOBEGTMISVFDSAII!AFNPRKLVLRVLKAYND
RVRDAGGIALVTYTAGVADEDIEEEIPGLFDVHIQMOGSVISAVMDGERTEAPYMITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(7122. .7823)
/gene="MTH593"
/forde="Function Code:14.01 - Unknown, Conserved protein;
/milar to, pir:LN:F64469 AC:F64469, p()=4.2E-12, pid=28%"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLVYLFTEWDYEPELIDKIRESMDCVVNLRTIEERVIIGQGFWVANSAWSEPPSTWVL
FYVOPGGGVRYVYVRILVTGPYNSGKSSFVRALATKSVSVDRALSAPFTIAMDIGH
LEYKGFWADIFGTFGOGREPDMILDVLSREAYGAFILLDSTAPETFARKEMIRKTRAE
AIPKVVVANKQDLFGALSPEEIREMWKLGADVPIVPASVTEGWGVRDALDTILGLLYG
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                                                                                                           /note="47 bp direct repeat includes part of MTH592
(conserved protein - paralog.fam. 32); 100% ID to interval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Function Code:14.01 - Unknown, Conserved protein; similar to, gp:GI:e198926:g1103582, p()=7.2E-10, pid=12%" /codon_start=1 /transl_table=11
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                    /note="47 bp direct repeat includes part of intergenic sequence ); 100% ID to interval 532261-532215" complement(6430. .6476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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90.0%; Pred. No. 91;
ive 0; Mismatches
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                                                                                                                                                                                        complement(6446. .7120)
/gene="MTH592"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(7122. .7823)
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                                                                                                                                                                                                                                                 complement(6446. .7120)
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                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="MTH593"
                                                                                                                                                                532193-532147
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repeat_region
                                                                                repeat_region
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Matches 1
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gene="MTH589"

/note="Function Code:14.01 - Unknown, Conserved protein;

similar to, pir:LN:B64484 AC:B64484, p()-8.9E-10, pid=28%"

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RRYLDALEELGVNVSPVKRIGRPRKYTDNDVKLVQSLLKEGKTPKQISGITNIPLKTV
YYLKGDIKLKRGKKRKYDRNTRLRVREMARNGMPARKISKDLGIPLRTVYYILKNG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="N-acetylglucosamine-1-phosphate transferase"
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/db_xref="GI:2621669"
/db_xref="GI:2621669"
/translation="MPDYVYGDSMVLKLTLEYSSVLLVSLICCIIAFTSTYTVMPRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NMLAGLNGIESGLGSIAMTALTASCIIMGKYDVSIITMAMLGALLAFLMYNRYPSRVF
PGDVGTLIIGACIASVAFIGRVKIIALIVLLPNIIDGILKFYSAGVVERHKHRPTEIA
EDGKLIAPPEGFNSLIRWILRRPMTEKKVVMIVWSIGMFFGFLGVLLAFILPLDPF"
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AGFY AEGGOTREALDYLERAYRVASEMNDEELMAFALDSMGDYTLSDRKVKTAMEYEM
AGFY AEGGOTREALDYLERAYRVASEMNDEELMAFALDSMGDYTLSDRKVKTAMEYEM
EARLYTSVNSPLRADLERAYREVEYR TREAMDIASINRLREESESGMPEVDLEVIEPL
LNRLVDSVQSLILVFRAGSYEDSISOIMEAYQIARDIGDTSTEASLQILLGIYSLKNED
FDESRRYLKKAEFARTNNELGLAVALVLLGTLDFIRNNADGVASSFRAAVEILQKL
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LLVGIVGMVDDLVRLSSREKLFLLFLAGLPIIWVAPPKVGILYMIMMPVAVSIASNLT
                                                                                                                                                                                                                                                                                                    /translation="MNESGLIARSERFLESIKDRKVSLDDLKSVEGFIDLYTYLRGNL
EELQDLKEAMELRGFKYPFRSISGYSSQYSPEIAEDVHDIKRHAQYFRMKASTKKNLL
DRVNSAISSHRIALGNLEEYALLQCPDCSRSLRLSEVEYQDILDGVMCPCGSGRMEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALGYAGLSHDIIMDIKERVYSEKLRDYDAVKRYRRILFEARTYSPOLRLSEDELQEVR
VQKMHDLLHEAGLGDSGGRLNRELREDLEVMEEVKRELFRDVPVNLVLMDVALYYLGT
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KVLEDGRWIRRRITIDSDDNDYERMLRQRYGPNVRIELIQFHRKKSSIINDRYTRTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KFEIEDKMKGLHMKPNPLAFGAAVLHMEGEADIETCAEIFHVRVEEVVEEKRNIENLG
KPSTDRAKMFLNLIKGD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Function Code:11.02 - Cell envelope, Surface polysaccharides; similar to, pir:IN:H64438 AC:H64438, p()=4.4E-40, pid=27%"
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/db_xref="PID:92621668"
/db_xref="GI:2621668"
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/protein_id="AAB85094.1"
/db_xref="PID:92621667"
/db_xref="GI:2621667"
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/gene="MTH590"
4323. .5321
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                                            /gene="MTH588"
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                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
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AUTHORS
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COMMENT
                                                                                                                     ACCESSION
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                                                                                                                                             VERSION
KEYWORDS
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                     g
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VAGIDLKTNKVVWQHRNGTLRDSMYGSSLPIPLPPIKIGVPSLGGPLGTAGNLGFLTA
SMDYYIRAYNLTTGKVLWQDRLPAGAQATPITYAINGKQYIVTXAGGHNSFPTRMGDD
                                                                                                                                                                   Gluconobacter.

[ Jakes 1 to 2890]

Cleton-Jansen, A.M., Dekker, S., van de Putte, P. and Goosen, N.

A single amino acid substitution changes the substrate specificity of quinoprotein glucose dehydrogenase in Gluconobacter oxydans Mol. Gen. Genet. 229 (2), 206-212 (1991)
                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (07-FEB-1992) N. Goosen, Dept of Mol Genetics, Gorlaeus
Laboratories, Leiden University, P O Box 9502, 2300 RA Leiden, THE
                                                                                X67710.1 GI:58416
Coenzyme PQO: gdh gene; gluconic acid production; glucose
dehydrogenase; quinoprotein.
Gluconobacter oxydans
Gluconobacter oxydans
Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
                                   15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="mutation changing substrate specificity"
975 c 786 g 574 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.8; DB 1; Length 2890;
Pred. No. 71;
0; Mismatches 2; Indels 0;
                                  BCT
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .2890
1. Organism="Gluconobacter oxydans"
/db_xref="taxon:442"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="gdh"
/note="membrane spanning fragment"
2612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="glucose dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="gdh"
251. .2677
/gene="gdh"
/EC_number="1.1.99.17"
/codon_start=1
                                  DNA
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90.0%; Pred
0; )
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                         G.oxydans gdh gene.
X62710 S60040
g58416
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                  NETHERLANDS
                                                                                                                                                                                                                                                                             Goosen, N.
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                             LOCUS
DEFINITION
ACCESSION
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ORGANISM
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AUTHORS
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                    JOURNAL
    RESULT
GOGDH/c
                                                                                                 KEYWORDS
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                                                                                   VERSION
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Gaps

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Indels

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IPDAVDVLAVFVARAIVDDILPPAFILKKQMKLLPDNSKGVEVILRAEKSYLATPLHAE
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ESADDTALDNPVVVEDLAMFRARVVDSVLARPRESVLOSGEKYLOVAR
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                                                                                                                                                                                                                                                                                  712227.1 GI:2505864
GTP-binding protein; hypothetical protein; poly(A) binding protein;
ribosomal protein S18A: RPS18A gene; topoisomerase.
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Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

Rosidae; Capparales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Terryn, N., Neyt, P., De Clercq, R., De Keyser, A., Van Den Daele, H., Ardiles, W., Dehais, P., Rouze, P., Gielen, J., Villarroel, R. and Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(<2325. .2377,2471. .2497,2618. .2717,2816. .2962,
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                                                                                                                                                                                 07-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Terryn, N.
Direct Submission
Submitted (02-APR-1997) N. Terryn, University Gent, Lab of Genetics, VIB, K.L. Ledeganckstraat 35, 9000 Gent, BELGIUM 2 (bases 1 to 24053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Related sequences: Y09821, Y09822, Y09823, Z23165, Z28701
Location/Qualifiers
                                                                                                                                                                              DNA PLN 07-C
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                                                                                                                                                                        ATX12227 24053 bp DN
Arabidopsis thaliana DNA,
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intron

exon

exon

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VQQHIQQOQLMHRNPSPGMRYMNGASNGRNGMDSSVPQGILPPIIPLPIDASSISHOK
APLLPISKLTSSLASASPADRTRMLGEQLYPLVERHEPLHVAKVTGMLLEMDQAEILH
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Pred. No. 1.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6474 TGCCATTGATACGGTTCATC 6455
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90.0%;
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                        Shinn, P., Brooks, S., Buehler, E., Chao, Q., Dunn, P., Khan, S., Kim, C., Walker, M., Altafi, H., Araujo, R., Conn, L., Conway, A.B., Gonzalez, A., Hansen, N.E., Huizar, L., Kremenetskala, I., Lenz, C., Li, J., Liu, S., Luros, S., Rowley, D., Swattz, J., Toriumi, M., Vysotskala, V., Yu, G., Davis, R.W., Federspiel, N.A., Theologis, A. and Ecker, J.R., Genomic sequence for Arabidopsis thaliana BAC I10024 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-APR-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 89934)
Shinn,P., Brooks,S., Buehler,E., Chao,Q., Dunn,P., Khan,S., Kim,C., Balker,M., Altafi,H., Araujo,R., Conn,L., Conway,A., Gonzalez,A., Luros,S., Rowley,D., Schwartz,J., Toriumi,M., Vysotskaia,V., Yu,G., Davis,R., Eederspiel,N., Theologis,A. and Ecker,J.
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SFDNLDHHRNFSNPSSRGLSFLRLSVSSAFD"
6855. 6932,7008. 7297,7466. 7502))
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                                                                                                                                                                                                                                  Arabidopsis thaliana Streptophyta; Embryophyta; Tracheophyta; Bubryophyta; Tracheophyta; euphyllophyta; Spermatophyta; Magnoliophyta; eudicotyledons; coreedicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-MAR-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 89934)
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Submitted (17-JUN-1999) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA
On Apr 2, 1999 this sequence version replaced 9::4464282.
                                                      Genomic sequence for Arabidopsis thaliana BAC T10024 from
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/note="unknown; similar to EST gb|N96021"
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                                                                               Chromosome 1, complete sequence
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                                                                                                                                                        AC007067.4 GI:4558521
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2 (bases 1 to 89934)
Ecker, J.R.
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                        89934 bp
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This sequence is of BAC T22018 from Arabidopsis thaliana chromosome insert of this clone. It is shorter by 11541 bp because we submit only the unique sequence of the clone. However, in order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide a small overlap (200 bp) between overlapping submitted clones. The 5' end of this sequence overlaps by 200 bp the 3' end of the sequence of the BAC F19610.
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VPQVLRNSRHGISHGQLYERFRELLERGOGTHERUEY
                                                                                                                                                                                                                                                                                                                                                                  Vysotskala V.S., Schwartz, J.R., Toriumi, M., Yu, G., Oji, O., Kwan, A., Liu, S., Li, J., Araujo, R., Au, M., Brendel, V., Buehler, E., Conway, A.B., Conway, A.R., Dewar, K., Feng, J., Kim, C., Kurtz, D., Li, Y., Palm, C.J., Shinn, P., Sun, H., Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A.
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YLSGVFASIVTWNTIAGGCLEAGNYIGALNCVVGMRNONVRIGSYBAMINGLKACSHIG
ALKWGKVFHCLVIRSCSFSHDIDNVRNSLITWYSRCSDLRHAFIVFQQVEANSLSTWN
SIISGFAYNERSEETSFLLKEMLLSGFHPNHITLASILPLFAR"
                                                                                         Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
1 (bases 1 to 83163)
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complement(<88..1372)
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complement(<88..1372)
/gene="722J18.1"
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A. thallana BAC gb|AF007269. EST gb|F14461 comes from
this gene. Gene continues on the 3' end of BAC F19G10
gb|AF000657 gene F19G10.21."
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The sequence of BAC T22J18 from Arabidopsis thaliana chromosome 1. Location/Qualifiers 1. 83163

1. 83163

Agranian Arabidopsis thaliana
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Submitted (07-3AN-1998) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 83163)
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Submitted (02-UNN-1998) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 83163)
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/gene="T22J18.2"
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/gene="T22J18.2"
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/evidence=not_experimental
/evidence=not_experimental
/product="110024.8"
/p
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CKUPPTOASUSDETSALSRPONTERENINVATTALDELINGETIMARIDEGGGG
GVVPPHVPPRASEVTYCLDGYLLVGFYDTGGRYFTDELHPGETFYPFRGLIBFLYNID
TVSALANSGLSGNPGTQVSLSSFRSPPFLYCVLKKSKANDINGOPVARIRKSLEG
complement(join(23710 . 24085, 24185 . 24255, 24338 . 24415,
24503 . 24579, 24668 . 24845))
Anote—'Similar to response regulator 1 (dbj|BAA311431);
similar to ESTS gb|T43772, emb|Z34204, gb|AA067391, and
emb|Z34620"
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                                          complement(20664. 21317)
/note="similar to germin-like protein (gi|2935521);
similar to ESTs gb|T88481 and gb|A1099566"
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/note="putative zinc finger protein 5 (pir(S55885)"
AKVLNTGDHIGLFWDKLTREVKFKHFKSQSITMHREAGTTSTQKNVLQKK"
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30820. .31455
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Best Local Similarity
Thes 18; Conserva
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AC003979
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TEQQNGDTERNCLSKATTSGSPTSEPKAGSPTQHERKPLRPLSPWISDILLAAPLGIR
SDYFRWCSGVMGKYAAGELKPPTIASRGSGKHPQLMPSTPRWAVANGAGVILSVCDDE
                                                                                                                                                                                                                                                                                       VARKETATLTAVAVPALLLPPPTTSLDEHLVAGLPALEPYARLFHRYYAIATPSATQR
LLLGLLEAPPSWAPDALDAAVQLVELLRAAEDYASGVRLPRNWMHLHFLRAIGIAMSM
RAGVAADAAAALFRILSQPALLFPPLSQVEGVEIQHAPIGGYSSNYRKQIEVPAAEA
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TLGSCKVAMDYTGRSKGYGFVOPERESBAQAALDKLMOMLMNRGVFVGHFIRRDERA
RDENTPTPRTNUYVKRLDYREIGEDELRKTFGKFGVISSAVVNRDOGGNSRCFGFVUR
ECTEAAASAVEKMNGISLGDDVLYVGRAQKKSEREEELRRKFEGERINRFEKSGGANL
YLKNDDDSVDDEKLREMFSEYGWYTSSKVMLNPGGMSRGFFYAYSNRPEELRRLSEM
NGKMIGRRPLYIALAGREDBRAHLQIRAPGPPROGNSGFPAYSONPEELREALSEM
NGKMIGRRPLYIALAGREDBRAHLQIRAPGPPROGNSGFPAYONGONGA
SWVPSQPIGYGFQPOFMPGMRPGSGFONFIVPYPLQRCPPUGFPRGFRRGAINVQQHI
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ISKLISSLASASPADRTRMLGEQLYPLVERHEPLHVAKVTGMLLEMDQAEILHLMESP
EALKSKVSEALDVLRLSVDPTDHDLGFSTTD"
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THPNSSL7AGDLDPKVTEAHLFDLFKHVANVVSVRVCRDQNRRSLGYAYINFSNPNDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(19494. 19709,20074. 20289,20361. 20642,20749. 20838,20925. 21002,21095. 21476,22391. 22694))
//gene="record of the content of
translation-"MASSSSERWIDGLQFSSLLWPPPRDPQOHKDQVVAYVEYFGQF/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSU46025 2898 bp DNA PRI 08-JAN-1999
Human translation initiation factor eIF-3 pl10 subunit gene,
complete cds.
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Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2898)
Asano,K., Kinzy,T.G., Merrick,W.C. and Hershey,J.W.
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26180. .26231,26320. .26463,26737. .26838,26932. ..
27094. .27145,27249. .27382))
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/protein_id="AAC25510.1"
/db_xref="PID:93287682"
/db_xref="GI:3287682"
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/gene~"T22J18.8"
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8571. .8584))
/gene="T22J18.4"
/codou_start="122J18.4"
/codouct="T22J18.4"
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FTATDPISFREVTLSLLEFCVLNINUMLYLYLJGEDEGGGIGILGGGGTFSPLK
FTATDPISFREVTLSLLEFCVLNINUMLYLYLJGEDEGGGILGGGGSGGEFSPLK
VEDVQQCHREISSPECVVVSERGKDDISEADNGSSREAFKLSLRSSIKRPSVAESRS
LEDIKEYTLSVDGSDLTGDMARRNVQWPDACGSELTQVREFERRY"
/gene="T22J18.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(41%) .4351,4543 .4697,4798 .4885,
4966 .5044,5144 .5208,5308 .5377,5489 .5630,5706 .5748,
5903 .5986,6082 .6273))
/gene="722J18.3"
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//protein_id="AAC25509.1"
//protein_id="PID:91287681"
//db_xxef="01:3287681"
//db_xxef
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TMDKLRDDDLERLKKIRNHRGLRHYWGLRVRGOHTKTTGRRGKTVGVSKKR"
COMplement (11397. .15895)
/gene="12218.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(11397. 11681,11983. 12051,12164. 13596,
13797. 14006,14133. 14283,14410. 14647,14817. 14872,
15019. 12290,15375. 15517,15560. 15650,15731. 15895))
/gene="T22J18.6"
                                                                                                         /note="ESTs gb|z34075, gb|z34835 and gb|AA404888 come from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jobe - Match to ribosomal S18 gene mRNA gb[228701, DNA gb]223165 from A. thaliana. ESTS gb[721121, gb]217755, gb]R64776 and gb]R30430 come from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(9130. .9235,9562. .9690,9956. .10116,
10301. .10303))
/gene="T22J18.5"
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TKRVYKSAKKRKRKRREELTLIRTIKMAMKIRDYTKCLEFFELLGRAKKKSIVDKEGY
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2 (bases 1 to 2898)
Asano,K. and Hershey,J.W.B.
Direct Submission
Submitted (12-JAN-1996) Katsura Asano, Biological Chemistry,
University of California at Davis, Schoo! of Medicine, Building
MSIA, Davis, CA 95616, USA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 156641)

Adams,M.D., Loftus,B.J., Zhou,L., Crosby,M., Fuhrmann,J.,

Mason,T.M., Brandon,R., Kim,U.J., Kerlavage,A.R. and Venter,J.C.

Unpublished
Conservation and diversity of eukaryotic translation initiation
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                                                J. Biol. Chem. 272 (2), 1101-1109 (1997) 97150873
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90.0%; Pred. No. 71;
tive 0; Mismatches
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Adams, M.D. and Loftus, B.J.
Direct Submission
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Direct Submission
Submitted (14-JUL-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
Medical Center Dr., Rockville, MD 20850, USA
On Jul 24, 1998 this sequence version replaced gi:2959563.
Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: humgen@tigr.org. The orientation of the sequence is from SP6 end to 77 end. Genes were identified by a combination of five methods including: XGRALL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Mashington), Genscan (Chris Burge, http://gnomic.stanford.Edu/-chris/GenscAmw.htm))searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete sequence against a peptide database, and the Human gene Index database at TiGR (http://www.tigr.org/tdb/hqi/hqi.html). Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE).

1. 156641
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PRFYIRILADLEDYLNELWEDKEGKKKMNKNNAKALSTLRQKIRKYNRDFESHITSYK
ONPEGSABDEDAEKNEEDSEGSSEDEDEDGVSAATFLKKKERPERSRKELKKMDDE
DEDSEDSEDDEDWATGSTSSDSDSEBEEGKOTALASFLKKAPTTDEDKKAAEKKRED
KAKKHDRKSKRLDEEEDDNEGGEWERVRGGVPLVKRFKMATGTTSTHAVVIKKLN
EILQARGKKGTDRAAOIELLQLLVOITAAENNLGEGYIVKIRFNIIASIYDYNNLATY
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MDEEFTKIMONIDPHSQEYVEHLKDEAQVCAIIERYORYLEEKGTTEEVCRIYLLRIL
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CAILCHIYHHALHSRWYQARDLMLMSHLQDNIQHADPPYQILYNRTWYOLGICAFROG
LTKDAHNALLDIQSSGRAKELLGQGLLLRSLQERNQEQEKVERRRQVPFHLHINLELL
ECYYLVSAMLLEIPYMAAHESDARRRMISKQFHHQLRVGERQPLLGPPESMREHVVAA
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33358. 33423,33522. 33861,35998. 36361,40957. 41181,
41407. 41597,43190. 43283,4419. 43544,43739. 43880,
44649. 44752,44877. 45036,52772. 52899,53278. 53387,
53516. 53570,53760. 53885,54108. 54297,54440. 54505,
//gene=*A-761H5.1*
Submitted (12-SEP-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA, Email: madams@tigr.org 3 (bases 1 to 156641) Adams,M.D. and Loftus,B.J.
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2796ne-A,761H5.3"
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/db_xref="taxon:9606"
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/map="16p11.2"
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27383.
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CLUNIESYVVMLGAMPILSHKRYGGNOSHVDGPPPIPHNSSRFDCNSVSTAAVLL
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IPALLLASYFLLISPEAQDPGGEEREASARQPLIRTEAPESKFGSSSSISLRERWT
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SSLRCCRIRFTWALALLQCLNLVFLLADVWFGFLPFYYFLIILYFGLLGGAAVVNT
FHNIALETSDEHREFAMAATCISDTLGISLSGLLAPLHDFLCQLS"

38891 c 38211 g 37878 t 59 others
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Eutheria: Primates: Catarrhini: Hominidae; Homo.

1 (bases 1 to 150296)

S Adams.M.D., Loftus.B.J., Phillips,C.A. and Venter,J.C.

Direct Submission

L Submitted (04-MAR-1997) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

E (bases 1 to 150296)

S Adams.M.D., Loftus.B.J., Zhou,L., Venter,J.C., Phillips,C.,
Brandon,R., Fuhrmann,J. and Kim,U.J.

L Submitted (10-ARP-1997) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, Maryland 20850, USA

E 3 (bases 1 to 150296)
                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MGGCAGSRRRFSDSEGEETVPEPRLPLLDHQGAHWKNAVGFWLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA PRI 22-OCT-1998
BAC clone CIT987SK-A-234F9, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-JUL-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA BAC clone CIT987SX-234F9 is located in band 16pll.2 of chromosome 16. Genes were identified by a combination of five methods: XGRAIL (available by ano nymous ftp from arthur.epm.ornl.gov), Genefinder (available by
             .135571,
.139505,
.140756,
.144570,
                                                                                                                                                                                                     .135571,
.139505,
.140756,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 156641;
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0
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135131. 13524,13533. .135408,135503. .1.
135652. 135698,137020. .1373132,139362. .1.
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141006. .141677,142305. .142401,144492. .1.
144774. .144769)
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.137132,139362.
.140556,140677.
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90.0%; Pred. No. 1.6e+02;
live 0; Mismatches 2;
                                                                                                                                     complement(<130544. .144946)
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                                                                                                                                                                                                                                                                                                                                                   /product="CLN"
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Best Local Similarity 90.0°
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Direct Submission
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YDSISMETLSDMFELDLPTVHSIISKMIINEELMASLDQPTQTVVWHRTEPTAQONLA
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THRANLERWORDARVELMEGPOKEKEELDRGCWERVELME
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEWILHEELSWECKLEEMPKKKEMTWNVDTLSKSSFRLGEMDPTKAKFPWQOCIDAGLR
VPNSEVSEAKEGEEECSGTGCWKLFPRQAGMSVRDPPQLQLPPVCKPLGAPFQKTKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MRLRFWLLIWLLLGFISHOPTPVSFLKTIFWSRNGHDGSMDVOO
RAWRSNXSRQKGLRSICMHTKKRVSSFRGNKIGLKDVITLRRHYETKVRXKIRKRKVT
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AFEHSLPGGDMDTFFSLQLCAQALQREMAERKAAYRHHSPIPVGNRVVOKHLHPHPVG
                                                                                                          /note="7608, STS1-cSRL-24g1-uA/cSRL-24g1-uz, Chr. -, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(110411. .>123468)

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yene="A-761H5.2"
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                                                                                                                                   sapiens"
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Eiglmeier,K., Honore,N., Woods,S.A., Caudron,B. and Cole,S.T.
Use of an ordered cosmid library to deduce the genomic organization
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The New York Community Trust.

Work in Paris is supported by the Heiser Trust, the Association Francaise Raoul Follereau and the Groupement de Recherches et des Etudes des Genomes (GIP-GREG).

Details of M. leprae sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/pathogens/)

CDS are numbered using the following system eg MLCB33.01c. ML (M. leprae), CB33 (cosmid name), .01 (first CDS), c (complementary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-APR-1997) Mycobacterium leprae sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrell@anger.ac.uk Cosmids supplied by Dr. Stewart T. Cole, [3] Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France Requests for cosmids should be sent to Karin Eiglmeier
         /note="7608, STS1-cSRL-24g1-uA/cSRL-24g1-u2, Chr. -,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acetyltransferase; cdp-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase; Coiled coil protein; glycosyl transferase; metE; methionine synthase; pgsk; ppdK; pyruvate phosphate dikinase; recA; REPLEP; sporulation protein. Mycobacterium leprae.
                                                               /db.zerf-"dbSTS:G02122"
145648. 145778
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146724. 146836
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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90.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 2;
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93188700
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Mycobacterium leprae cosmid B33.
294723
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Barrell, B.G. and Rajandream, M.A.
Direct Submission
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Badcock, K. and Churcher, C.M.
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Best Local Similarity 90.0°
Matches 18; Conservative
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                                              saptens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDSISMETLSDMFELDLPTVHSIISKMIINEELMASLDOPTOTVVMHRTEPTAQONLA
LOLAEKLGSLVENNERVFDHKQGTYGGYFRDQKDGYRKNEGYMRRGGYRQQOSQTAY*
105065. .105182
anonymous ftp from colineu.washing ton.edu), GENSCAN (available using the e-mail server at genscan@gnomic.stanford.edu), searches of the EST database at TIGR (http://www.tigr.org/tdb/hcd/hcd.html) and searches against a peptide d atabase. Repeats were identified using RepeatMasker (Smit, A.F.A. and Green, P. unpublished, http://tp.genome.washington.edu/rm/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43758. .43870
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43758. .44232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55657. _55762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /pseudo
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55657. .55762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(80543. .104718)
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gene

CDS

STS

mRNA

gene

STS

SIS

gene

FEATURES

STS

gene

CDS

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Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. All CDS over 100 codons have been analysed. Gene prediction is based on positional base preference in codons especially where there is an increase in the observed/expected third position G + C. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg. gtg. or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid #CONIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MLCB33.02c, possible glycosyl transferase, len: 392 aa, identical to Q49841 Q49841 U2235C except more upstream initiation codon chosen on the basis of similarity eg to CRIX_ERWHE COU330 zeaxanthin glucosyl transferase (413 aa), fasta scores, opt: 233, E(): 1.4e-07, (26.1% identity in 410 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MAQVPDREKALELAMAQIEKNYGKGSVMRLGDEMCQPISVIPTG
SIALDVALGIGGLPRGRIVEIYGPESSGKTTVALHAVANAQAVGGVAAFIDAEHALEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /traislation="MYHYMRYAVVAGPDPGHSFPAIALCQRFAEAGDTPTLFTGVECV
DIARAAGVETALLDGLVAVDDVDAGARIHRRAAQMAVLNVPVLRDLAPDLIYSDVIT
AAGGMAAELLGIPWIELNPHPLYLPSKGLPPIGSGLASGVGIHGRMRDATMRALTARS
WRAGLRERAAVRVQIGLPACDSGPLRRLIATLPALEVSRPDWPAEAVVVGPLHFEPTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="overlap with positions, 3000. .36033 EM_BA:ML019 u00019 Mycobacterium leprae cosmid B2235, note conflict with this sequence at the 5' end" complement(171. .194)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MLCB33.01c recA, (partial) contains PS00017 ATP/GTP-binding site motif A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="cagtc missing in entry EM_BA:ML019 U00019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(400. 404)
/note="aggag, potential rbs upstream of recA"
complement(760. .1938)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="recA"
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    .42224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SPTREMBL:005556"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(760. .1938)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref-"PID:e313312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1. .392)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="cosmid B33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement(3726. 4070)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"WPGIWPGDHSNAHVVYHAIAPLCHVSPKLVAIAELTEASVOGVE
NIRTVEVFLAALQDAGLRNRIRDVGRQPRVYONVGLPTIHGRSKTITLWRKMADCIGF
EIKIHRIAAVAIAVLCERADAVIVGPLWMQFWVCGTFEVQNKRIMLWRNYFDLFDLFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB08116.1"
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RQGSAQLIRPLTAAALLAAVNKVLSSPDYREAAQRAAISIAGVADPVQVCHEALGLAG
RVLQIPSGSGPVIVVAPSTALTGISGMAQTALDALVPGDTLPSGSRVVVSRLNGPDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4054. .4557)
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                                                                                                                                                                                                                                                                                                                                                                                           /note="MLCB33.03, unknown, len: 178 aa, identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="gaggig, potential rbs upstream of MLCB33.04c" complement(3726. 4070)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown, len: 123 aa, identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1946. .1949)
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complement(4054. .4557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3692. .3697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRSEPLPTWRPNGVRRLLPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                    049850 B2235_F3_140"
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FEATURES

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OM nucleic - nucleic search, using sw model

September 18, 1999, 05:27:15; Search time 213.04 Seconds (without alignments) 23.488 Million cell updates/sec US-09-037-472-3 20 1 TGGCATTGATCTGGTTCATC 20 Title: Perfect score: Sequence: Run on:

IDENTITY\_NUC Scoring table: 311585 seqs, 125096042 residues Searched:

N\_Geneseq\_36:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Name			ap (				
20 100.0 20 1 Y33391 Frimer for detection of the control of the co	ا و ب	Score	Vuery		DB	В	Description
20 100. 20 1 V32393   Interlaukin-1-box detections of the control	-	20	6		: :		
20 100.0 20 1 V60291 Printerleukin 1 (4 10.0 10.0 10.0 10.0 10.0 10.0 10.0 10.	ر ا	000			4 +	10000	ior detect
20 100.0 20 1 X16612   Interleukin 1 (46.8   46.0   10.0 1 0	4 0	9 6			٠,	V32391	rleukin-l-be
• 20 100.0 14690 1 X22995	) <b>&lt;</b>	9 0	3 8		٠,	V6U232	primer used
1.00   1.00	<b>†</b> U	0 0	9	,	٠,	XIBBIS	eukin 1 (4
16.8 84.0 2854 1 X22996 Human IL-Ira BAC 1 X22996 16.4 84.0 2854 1 V86039 16.4 84.0 2854 1 V86039 16.4 84.0 20246 1 V74367 Staphylococcus a V8603 15.4 77.0 3004 1 T12337 Mycobacterium sp. 15.4 77.0 3004 1 T12337 Mycobacterium sp. 15.4 77.0 714 1 X34151 Mycobacterium sp. 15.4 77.0 714 1 X34151 Mycobacterium sp. 15.4 77.0 714 1 X34151 Mycobacterium sp. 15.2 76.0 1073 1 M82405 Staphylococcus a Sta	<b>1</b> u	•	3 8	4 6	٠,	X22303	IL-1ra BAC
16.8   84.0   2584   1 V32591   1 Schwannomin-bind   16.8   84.0   2584   1 V32591   1 Schwannomin-bind   16.4   82.0   30246   1 V74367   1 State   1 V21461   1 State   1 V21461   1 State   1 S	01	٧,	3 8	7	٠,	X02996	Human IL-1ra BAC c
16.4   84.0   30.24   1	<b>~</b> c	٠,		282	щ,	V32591	Schwannomin-bindin
15.4 82.0 30246 1 V74357 Staphylococcus 15.8 79.0 2220 1 V21460 Rhodosporidium 15.8 79.0 2220 1 V21461 Rhodosporidium 15.8 79.0 2320 1 V21460 Rhodosporidium 15.9 79.0 3004 1 T12337 A. cellulolytic 15.4 77.0 3004 1 T12337 A. cellulolytic 15.4 77.0 3004 1 T12337 A. cellulolytic 15.4 77.0 174 1 X34127 Mycobacterium s pGTR200-DNA ins 15.2 76.0 1233 1 N82405 PGTR200-DNA ins 15.2 76.0 1223 1 N82405 PGTR200-DNA ins 15.2 76.0 1222 1 Q22205 Rat Diver gluta 15.2 76.0 1222 1 Q22205 Rat Diver gluta 15.2 76.0 1222 1 Q42205 Rat equilibrea extiv 15.2 76.0 12000 1 T58840_4 Sat dequilibrea for firefilles 14.8 74.0 12078 1 V22203 Rat equilibrati 16.8 74.0 12078 1 V22203 Rat equilibrati 16.8 74.0 12078 1 V22203 Rat Rat CAD Enzym 14.8 74.0 12078 1 V22203 Rat Rat CAD Enzym 14.8 74.0 12078 1 V22203 Rat Rat CAD Enzym 14.8 74.0 12078 1 V22203 Rat Rat Rat CAD Enzym 14.8 74.0 12078 1 V22203 Rat Rat CAD Enzym 14.8 74.0 12078 1 V22203 Rat Rat Rat CAD Enzym 14.8 74.0 12078 1 V22203 Rat	o c	٠,		55	н,	V86039	38.
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SSULT 1  13885  113885  113885  113885  113885  113885  113885  113885  113886  114886  115886  118886	Secretion enhancin Strawberry inverta	ALIGNMENTS	position to periodontal disease.  riodontitis: polymorphism:  ukin-1 beta; IL-1B; primer; PCR;  disease severity  can be used in a new method  ition to periodontal disease by  intorin to periodontal disease by  orphisms in the gene sequences  interleukin-1 beta (IL-1B).  ase were identified as IL-1A  allele 2. The primers are used  to determine the polymorphism  d using primers (T13885 and  to -682 and -417 to -397,  allele 2 (T).  5 G; 8 T;	Score 20; DB 1; Length 20; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;	682). R; primer; amplification; thy; interleukin-1-alpha; ; ss.
RESULT 1 113885 standard; DNA; 20 BP AC 13885; tandard; DNA; 20 BP AC 13997 (first entry)  E Primer for detecting genetic particulary and polymerase chain reaction; Synthetic.  NOYOGAGE AL.  D 20-FEB 1997.  C 2-AUG-1995; U12455.  D 20-FEB 1997.  A MEDI - MEDICAL SCI SYSTEMS ACTION AND ACTION AC	N50411 T68694	ALIC	c prediscriptions per prediscriptions per	Score Pred. 0; Mis	(-702/- ism; PC etinopa kin-lRN Ki
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29-APR-1999 (first entry)
Interleukin 1 (44112332) haplotype PCR primer #9.
Interleukin 1; IL-1; haplotype; inflammatory disorder; alopecia areata; coronary artery disease; osteoporosis; nephropathy; diabetes mellitus; Graves disease; systemic lupus erythamatosus; lichen sclerosis; ulcerative colitis; PCR primer; ss.
              1 TGGCATTGATCTGGTTCATC 20
                                                                                                                                                                         X16615 standard; DNA; 20 BP
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21-MAY-1998, G01481.
29-MAX-1997; GB-011040.
(CAMP/) CAMP N J.
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                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                of mind 2: Page 33; 41pp; English.

Interleukin 1-beta (Ir-1-beta) primers 1 and 2 (V32392) were used to maplify the IL-1-beta gene region to identify single base variation polymorphism of C/T at base 51.

The mathod for predicting the risk of sight threatening diabetic retinopathy. The method for predicting the risk of sight threatening diabetic retinopathy. The method for predicting DNA from a patient and determining the DNA polymorphism pattern of the genes that code for in erleukin-1-alpha, interleukin-1-beta and interleukin-1RN. The polymorphic pattern of patterns thereby identifying patients carrying a genetic polymorphism associated with increased risk of sight threatening diabetic retinopathy. The method may be able to identify diabetic patients at risk before the clinically detectable disorders occur. Polymorphism pattern of IL genes involved PCR reactions using primers v32389. We method is also claimed to be useful in conjunction with retinopathy in genomic DNA and therefore, in identifying diabetic patients expressing multiple risk patterns.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Predicting increased risk of sight-threatening diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comparative measurement of levels of expression of alleles from the interleukin 1 locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 15; 22pp; English.

PCR primers V60232-33 were used to amplify alleles associated with interleukin-18 [L-18]. The specification describes a method for determination of a patient's predisposition to coronary arrery disease. The method comprises comparing an allele with a second allele which is predictive of coronary artery disease, where similarity between the first and second alleles indicates a

    comprises identifying genetic polymorphism pattern for genes
    IL-1A, IL-1B and IL-1RN, useful to allow treatment before clinical

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25-NOV-1998 (first entry)
PCR primer used to amplify interleukin-1B (IL-1B).
Interleukin-1B; IL-1B; predisposition; coronary artery disease;
Screen; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB 1; Length 20; Pred. No. 0.24;
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10-MAR-1997; US-813456.
(MDDI) MEDICAL SCI SYSTEMS INC.
Crossman DC, Duff GW, Francis SE;
WPI; 98-520829/44.
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100.0%;
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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While you would be determining a patient's susceptibility to inflammatory disorders - by detecting the presence of an IL-1 (4411232)

The proper, useful in designing treatment strategies that modulate the activity of proteins produced by the IL-1 gene cluster

Claim 3; Page 33; 49pp; English.

Ca method has been developed for determining a patient's susceptibility to an inflammatory disorder. The method comprises the detection of an internation of IL-1) (44112332) haplotype in a sample obtained from the patient, where its presence indicates susceptibility to an inflammatory disorder. X16607 to X16631 represent PCR primer used in the method for detecting the IL-1 (44112332) haplotype. The method provides kits for the early prediction of a patient's susceptibility to inflammatory disorders, including coronary artery disease, osteoporosis, nephropathy of indiabetes mellitus, alopecia areata, Graves disease, systemic lupus cervithmantosus, lichen sclerosis and ulcerative colitis. The detection of alsorders, comprising diabetic retinopathy, juvenile chronic arthritis, allohers can be applied to particular inflammatory disease-associated haplotype enables determination of which alleles are causative, and this information is useful in designing treatment using various agents causative, and this information is useful in designing treatment contacter the activity of proteins produced by the IL-1 gene cluster are associated with particular centrally in the pathology of these diseases. Therefore, the use of IL-1 centrally in the pathology of these diseases. Therefore, the use of IL-1 centrally in the pathology of these diseases. Therefore, the use of IL-1 centrally in the pathology of these diseases. Therefore, the use of IL-1 centrally in the pathology of these diseases. Therefore, the use of IL-1 centrally in the pathology of these diseases. Therefore, the use of IL-1 centrally in the pathology of these diseases. Therefore, the use of IL-1 centrally in the pathology of these diseases. Therefore, the use of IL-1 central 
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22-JUN-1999 (first entry)
Human IL-1ra BAC contiguous DNA sequence 96.
Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 G;
(COXA/) COX A.
(DGIO/) DE GIOVINE F S.
(DUFF/) DUFF G.
Camp NJ. COX A, De Giovine FS, Duff G;
WPI; 99-080814/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X22303 standard; DNA; 14690 BP.
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Best Local Similarity 100.
Matches 20; Conservative
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ID X223(
AC X223(
DT 22-JT
DE Human
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Query Match Best Local Similarity 100. Matches 20; Conservative

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Gaps

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While you isolated nucleic acid encoding the new human cytokine Tango-77 - 18 we isolated nucleic acid encoding the new human cytokine Tango-77 - 18 weed to inhibit inflammation and to screen for specific modulators by Example 5; Figure 4; 226pp; English.

X02956-X03048 and X2230-X22304 are overlapping BAC genomic sequences containing alternatively spliced forms of human In-Ira. Such fragments of are used in the method of the invention which describes the isolation of a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a sociated with acute or chronic inflammation by binding to the interleukin-1 receptor in processes associated with acute or chronic inflammation, e.g. asthma, chronic syclopage of the cytokines and growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of inflammation, or activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid encoding the new human cytokine Tango-77 - used to inhibit inflammation and to screen for specific modulators
Example 5; Figure 3; 226pp; English.

X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences
Containing alternatively spliced forms of human IL-Ira. Such fragments
are used in the method of the invention which describes the isolation of
are used in the method of the invention which describes the isolation of
are used in the method of the invention which describes the isolation of
an novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a
containing alternative superfamily that is expected to inhibit
containing to the interleukin-1 receptor (IL-IR). It may
contained with acute or chronic inflammation, e.g. asthma, chronic
myelogenous leukaemia, rheumatoid arthritis, psoriasis and inflammatory
containing also induce or suppress interleukins, cytokines and
containing actors. Modulators of this protein are used to treat or prevent
interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human IL-1ra BAC contiguous DNA sequence 41. Ango-77 human: IL-1ra; cytckine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; requlation; asthma; rhemmatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
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                                                                                                                                                                                  04-AUG-1997; US-054646.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Pan Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL-1 or its receptor complex. quence 14690 BP; 3810 A;
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                                                                                                                                       03-AUG-1998; U16102.
02-JUL-1998; US-091650.
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03-AUG-1998; U16102.
02-JUL-1998; US-091650.
04-AUG-1997; US-054646.
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Best Local Similarity
Matches 20; Conserv
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                                                                       Homo sapiens.
WO9906426-A1.
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WO9906426-A1.
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Py PyBDB; WayB928.

New nucleic acid encoding schwannomin-binding protein - useful for, e.g. diagnosis and treatment of brain tumours and in drug screening Claim 3; Page 53-57; 75pp; English.

This cDNA sequence encodes a human schwannomin-binding protein (SBP) (see W48928) that has been found to have functional involvement in the inititation of translation and is suggested to serve a role in the final steps of a signal transduction cascade from a human adult brain cDNA library using a yeast two-hybrid method with schwannomin isoform I as bait. Novel SBPs of the invention (see W48927-31) bind to the neurofibromatosis 2 (RP2) (Tom a human adult brain cDNA library using a yeast two-hybrid method with schwannomin, soform I as bait. Novel SBPs of the invention (see W48927-31) bind to the neurofibromatosis 2 (RP2) (Invention (see W48927-31) bind to the neurofibromatosis 2 (RP2) cargets for treating a broad variety of cancer pathologies, such as glioma, sarcoma, melanoma and hamartoma. They provide tragets for treating a broad variety of cancer pathologies, such as glioma, carcinoma, sarcoma, melanoma and hamartoma. SBPs are used of notein. SBP nucleic acids, oligonuclectides (including antisense), vectors containing these, transformed host cells and SBP polypeptides and antibodies of the invention can be used to screen for potental cardanning these, transformed host cells and SBP polypeptides and antibodies of the invention can be used to treat brain twell as cataracts and retinal disorders. Oligonucleciacides that cumours, such as glioma, schwannoma, meningioma and ependymoma, as the secretary of the invention can be used to treat brain twell as cataracts and retinal disorders. Oligonucleciacides that colds are used to identify or quantify nucleic acids are used to inhibit SBP expression. Single-stranded primars expressing exogenous nucleic acids are also claimed. Transgenic containing expressing exogenous nucleic acids are also claimed. SBP uncleic acids processing experience and for drug screening.
conditions associated with abnormal levels of inflammation, or activity of IL-1 or its receptor complex. Sequence 10620 BP; 2746 A; 2407 C; 2411 G; 3049 T;
                                                                                                                                                                             Gaps
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Schwannomin-binding protein cDNA.
Schwannomin-binding protein, SBP; human; neurofibromatosis 2;
Schwannomin-binding protein; SBP; human; neurofibromatosis 2;
NF2; tumour suppressor protein; brain tumour; glioma; schwannoma; meningioma; sarcoma; melanoma; ependymoma; cataract; hamartoma; cell proliferation; transgenic animal; signal transduction; Homo sapiens.
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                                                                                                                             DB 1; Length 10620;
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                                                                                                                        100.0%; Score 20; DB 1;
100.0%; Pred. No. 0.56;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-1998.
14-NOV-1997; U21005.
15-NOV-1996; US-030987.
(CEDA-) CEDARS SINAI MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                V32591 standard; cDNA; 2854 BP.
                                                                                                                                                                                                                                           6360 TGGCATTGATCTGGTTCATC 6341
                                                                                                                                                                                                                 1 TGGCATTGATCTGGTTCATC 20
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                                                                                                                                                                        Conservative
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                                                                                                                                              Similarity
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Matches 18; Conserv
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Matches 20;
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    DE 27-RP1-1999 (Intest entry)

EXT clone B238.

KW Expressed sequence tag; secreted protein; haematopoiesis regulator;

KW tissue growth; activit; inhibin; tumour inhibitor; Expressor; EST; human;

KW teeptgr; ligand; anti-inflammatory; tumour inhibitor; ds.

KW ceeptgr; ligand; anti-inflammatory; tumour inhibitor; ds.

KW osaphens.

NO SAPE-1998 (106954.

PT 10-APR-1998 (106954.

PT 10-APR-1998 (106954.

PT 10-APR-1998 (106954.

PT 10-APR-1998 (106954.

PT 10-APR-1999; USB TINC.

PT 10-APR-1999; USB TINC.

PT 30-APR-1998 (106954.

PT 40-APR-1998 (106954.

PT 40-APR-1998 (106954.

PT 50-APR-1998 (106954.

PT 60-APR-1998 (106954.

PT 60-APR-1998 (106954.

PT 80-APR-1998 (106954.

PT 80-AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus contig SEQ ID #56.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 14
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1741. .1800
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90.0%;
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                                                                                                                                                                             standard; cDNA; 558
                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 90.0
Matches 18; Conservative
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are included to maintain the nucleotide numbering
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Wri: y# Council for identifying bacteria causing infectious disease - consists of a DNA fragment obtained by HindIII cleavage of the pathogenic bacterial genomic DNA expension of the claim 7: Page 78-82: 100pp; Japanese.

The nucleotide sequence of a 6914 bp probe obtained by digestion of Enterobacter cloacae genomic DNA with the restriction enzyme HindIII. The probes (055133-48 and 055752-58) represent other probes derived, by HindIII digestion of the genomes of Staphylococcus aureus, S. epidemia, Enterococcus faecalis, Pseudomonas aeruginosa, E.coli, Klebsiella pneumoniae or Enterobacter cloacae. The probes can be used to detect their respective microorganisms in clinical samples. Sequence 6914 BP; 1420 A; 1937 C; 1807 G; 1750 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-1998 (first entry)
Rhodosporidium toruloides cephalosporin esterase genomic DNA.
Cephalosporin esterase; antibiotic; ds.
Rhodosporidium toruloides strain ATCC 10657.
                                                                                                                                                                                                                                                                                                            DB 1; Length 6914; 48;
                                                                                                                                                                                                                                                                                                                                              0; Indels
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/note= "contains 5 introns"
                                                                                                                                                                                                                                                                                                                                              Mismatches
                     Ohno T, Uehara H;
                                                                                                                                                                                                                                                                                                            Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                    80.0%;
100.0%; Pre
0; }
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V21461/c
TD V21461 standard; cDNA; 2220 BP.
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1377. .1439
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1440. .1652
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951. .1283
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695. .757
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Best Local Similarity 100.
Matches 16; Conservative
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                     Matsuhisa A,
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11-SEP-1997; U16193.
                                    WPI; 94-035086/04
     (OHNO/) OHNO T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents one of 5191 Staphylococcus aureus DNA sequences of this sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access nemory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the saureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a kit for the immunodetection of be used in a sample. S.aureus in implicated in numerous human diseases, including cellulitis, eyalid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences contained on the computer readable medium.
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                               the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence. 27000
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                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 97-374922/35.
Polynucleotide(s) and proteins derived from Staphylococcus aureus
stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-5EP-1995 (first entry)
Enterobacter cloacae genomic probe ET-49.
Probe: S.aureus; S.epidermis; E.faecalis; P.aeruginosa; E.coli; K.pneumoniae; E.cloacae; clinical sample; ds.
W09401583-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
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Q55757/c
ID Q55757 standard; DNA; 6914 BP.
AC Q55757;
AC Q55757;
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94.4%;
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07-JUL-1993; J00936.
07-JUL-1992; JP-179719.
(FUSO ) FUSO PHARM IND LTD.
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Best Local Similarity 94.4
Matches 17; Conservative
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                                                                                                                                            Claim 8: Fig 6A-B: 38pp; English.

Claim 8: Fig 6A-B: 38pp; English.

This nucleic acid molecule comprises genomic DNA of Rhodosporidium toruloides Arcc 10657 coding for cephalosporin esterase (see 1041059). It was isolated by using oligonuclectide probes (see 199709-12) based on the N-terminal sequence of the mature enzyme to recen Southern blots of R. toruloides chromosomal DNA. A cDNA clone (see V21460) is also provided. These isolated nucleic acid molecules can be used for the recombinant production of cophalosporin esterase using claimed expression vectors and claimed host cells (preferably Escherichia coll. R. toruloides.)

Cephalosporium acremonium or Penicillium chrysogenum). The cephalosporium esterase can be used for the hydrolysis of the 3' acctyl groups of cephalosporius. The polypeptide (even if catalytically inactive) can also be used for the production of catalytically inactive) can also be used for the production of antibodies for use in detection and purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                            Isolated cephalosporin esterase gene - obtained from Rhodosporidium toruloides, used to obtain products which can be used for hydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated cephalosporin esterase gene - obtained from Rhodosporidium toruloides, used to obtain products which can be used for hydrolysis of cephalosporins
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This cDNA clone codes for the cephalosporin esterase (see W54159) for Rhodosporidium coruloides ATCC 10657. It was isolated from total RNA of R. toruloides by first-strand cDNA preparation and amplification using a gene-specific primer and an adapter primer. A genomic DNA sequence (see V21461), which contains 5 introns, is also provided. These isolated nucleic acid molecules can be used for the recombinant production of cephalosporin esterase using claimed expression vectors and claimed host cells (preferably Escherichia coli, R. toruloides, Cephalosporium acremonium or Penicillium chrysogenum). The cephalosporin esterase can be used for the hydrolysis of the 3 acetyl groups of cephalosporins. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                              463 T;
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                               Burnett WV, Politino M, Romancik G, Tonzi SM, Usher JJ;
WPI; 98-230321/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-SEP-1997; U16193.
18-SEP-1996; US-026929.
(BRIM) BRISTOL-WYERS SQUIBB CO.
Burnett WV, Politino M, Romancik G, Tonzi SM, Usher JJ;
WPI; 98-230321/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V4140v;
17-AUG-1998 (first entry)
Rhodosporidium toruloides cephalosporin esterase cDNA.
Cephalosporin esterase; antibiotic; ss.
Rhodosporidium toruloides strain ATCC 10657.
Key
Location/Oualifiers
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                            554 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.0%; Score 15.8; I
89.5%; Pred. No. 52;
live 0; Mismatches
                     SQUIBB CO
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ID V21460 standard; cDNA; 1738
AC V21460;
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18-SEP-1996; US-026929.
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95...17
                   (BRIM ) BRISTOL-MYERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                  cephalosporins
                                                                             P-PSDB; W54159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; W54159
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New isolated uropathogenic E. coli nucleotide sequences - used to develop products for the detection of pathogenic E. coli and to elicit an immune response to pathogenic E. coli and to claim 21, page 224; 250pp; English.

Claim 21, Page 224; 250pp; English.

Claim 21, Page 224; 250pp; English.

Chis sequence represents a E. coli strain J96 contig containing pathogenicity island (PAL) sequences, and represents a nucleic acid molecule of the invention. Pals are large fragments of DNA which comprise pathogenicity determinants. The sequences of the invention are taken from the E. coli chromosome and is greater than 170 kb. PAI vo pal IV is located at approximately 94 min (at pheR) on the E. coli chromosome and is approximately 160 kb in size. Antibodies specific to the proteins encoded by the PAI open reading frames of the invention can be used in kits to detect uropathogenic E. coli. The proteins are used in vaccines to elicit a privatic immune response in an animal to the uropathogenic E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E. coli J96 pathogenicity island contig #112.
ARI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheV; vaccine; protective immune response; ds.
Escherichia coli.
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
polypeptide (even if catalytically inactive) can also be used for
the production of antibodies for use in detection and purification.
Sequence 1738 BP; 328 A; 639 C; 443 G; 328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-0cT-1996 (first entry)
A. cellulolyticus El endoglucanase gene.
El endoglucanase; cellulase; cellulose; saccharification; ethanol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/note= "base g at position 200 is shown in Fig 1,
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0
                                                                                                                                                DB 1; Length 1738;
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                                                                                                                                                                                                  Indels
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                                                                                                                                          Score 15.8; DE
Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.0%; Score 15.8; I
89.5%; Pred. No. 46;
tive 0; Mismatches
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Choi GH, Dillon PJ, Welch RA;
WPI; 98-312461/27.
                                                                                                                                          79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T12337 standard; DNA; 3004 BP
                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
AC V31298, standard; DNA; 930 BP AC V31298, coli 196 pathogenicity is DE COLT-1998 (first entry) DE C. Coli 196 pathogenicity is RW PAI; pathogenicity island; uN W0982257-A2.
BY ESCHARICHIA COLI.
PN W0982257-A2.
PR 21-NOV-1997; US-061953.
PR 14-OCT-1997; US-061953.
PR 14-OCT-1997; US-061953.
PR 14-OCT-1997; US-061953.
PR (HUMA-) HUWAN GENOME SCI INC (HUMA-) HUMAN GENOME SCI INC (HUMA-) HUMAN GENOME SCI INC PAI 199-12461/27.
PT Choi GH, Dillon PJ, Welch RA WPI 99-312461/27.
PT New isolated uropathogenic E PT develop products for the det C pathogenicity determinants.
CC pathogenicity determinants.
CC pathogenicity island (PAI) is CC aproximately 94 min (at phe CC approximately 94 min reasponse CC approximately 94 min response CC strain J96.
Sequence 930 BP, 319 A;
                                                                                                                                                                                                                                                                                                   746 TCGCAATGATCTGGTTCAT 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 A;
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                                                                                                                                                                                                                                              1 TGGCATTGATCTGGTTCAT 19
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                                                                                                                                  Query Match
Best Local Similarity 89.5'
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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ID T123

DT 08-09

DE A. C

KW EI el

KW ES.

OS Acid

FH Key

FT misc.
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Claim 4; Page 22-24; 34pp; English.

Claim 4; Page 22-24; 34pp; English.

Codes for an enzyme, the mature form of which (R89927) can hydrolyse collulose and xylan. The gene was obtd. by ligating Sau3A fragments of A. cellulolyticus genomic DNA into EMBL3 lambda phage arms, packaging the phage DNA, plating on E.coli LE392 agar contg. CMC, staining with Congo Red, and isolating DNA from positive clones. Alternative signal sequences were identified (see also R89928-29). The gene can be incorporated into a vector and used for large-scale, low-cost prodn. of recombinant El endoglucanase, pref. using Saccharomyces, Zymomonas or E.coli hosts. The enzyme is useful for the saccharification of cellulosic biomass for fermentation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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06-JUL-1999 (first entry)
Mycobacterium species nucleic acid sequence 29.
Secreted protein; Mycobacterium; primer; PCR; amplification; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated DNA encoding endoglucanase - obtd from Acidothermus cellulolyticus, used for prodn of the enzyme for use in cellulose
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                                      /*tag= b
/note= "putative upstream regulatory sequence"
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but is missing in the sequence given on page 22 of the specification"
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Pred. No. 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Laymon RA, Thomas SR;
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810. 817
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94.1%;
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824. .946
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863. .946
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27-JAN-1992; US-826089.
21-SEP-1993; US-125115.
15-JUL-1994; US-276213.
(MIDE ) MIDWEST RES INST.
                                                               772. .779
/*tag= c
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Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                                               signal_peptide
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                                                                                                                                                                                                                                                                                            mat_peptide
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                                                                                          repeat_unit
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                            misc_signal
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ID X34151
AC X34151
DT 06-JUL
DE Mycobac
KW Secret
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Gaps
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Claim 22; Fig 29; 309pp; French.
Sequences X34001-X34252 represent nucleic acids encoding secreted proteins from various Mycobacterium species microorganisms. The nuclectide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
Sequence 714 BP; 153 A; 212 C; 225 G; 124 T;
                                                                                                                                                                                         11-AnG-1998; F01813.
11-SEP-1997; FR-011325.
14-AnG-1997; FR-010404.
(INSP ) INST PASTEUR.
Gicquel B, Lim EM, Pelicic V, Portnoi D, Goguet de la Salmoniere Y,
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hybridisation; detection; vaccine; immunisation; infection; ss.
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Pred. No. 69;
0; Mismatches
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Best Local Similarity 94.1
Matches 16; Conservative
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WPI; 99-181045/15.
                                                             Mycobacterium sp.
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gb_est32:*
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gb_est20:*
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Perfect score:
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AA305985 EST176975
AA305985 EST176975
AA5060819 486072605
AL645670 DKF2p434A
AL645670 DKF2p434A
AL6459103 DKF2p434A
AL6459103 DKF2p434A
AL645910 Homo sapi
A1044531 Homo sapi
A1044531 Homo sapi
A104596 Homo sapi
A104596 Homo sapi
A104595 Homo sapi
A104595 Homo sapi
A104595 Homo sapi
A104531 CELK00199
D37412 CELK00199
D37412 CELK0045AX
R89462 9901010:r1
D65351 CELK00598R
W95680 Ze07105:s1
AA622988 Homo sapi
AA62298 Homo sapi
AA62298 Homo sapi
                                                              AA214464 zq89b01.r
A1365968 ao91c06.x
T27501 EST27i16 WA
T34213 EST64297 Hu
                                                                                                                                                                                    AA153319 ms6ic12.r
AA210873 zr88d07.r
C73486 C73868 Rice
A1044171 UT.R-C1-j
T08311 EST06202 In
T29096 EST68411 Hu
                                                                                                                                                                                                           R07242 yf14605.rl
R14146 yf78c01.rl
T77597 yc91e03.rl
T81887 yd34g11.rl
T85981 yd62d07.rl
T87073 yd88a09.rl
                                                         F07416 HSC25B041 n
                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                   Description
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                                                                                                    AI722423
HSM007819
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HSM010310
                                                             AA214464
A1365968
T27501
T34213
AA265846
AA305985
AA581691
A1600819
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AI614179
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C73686
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AL049103
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F07416 359 bp mRNA EST 20-FEB-1995 HSC25B041 normalized infant brain cDNA Homo sapiens cDNA clone c-25b04, mRNA sequence. F07416 g673074 F07416.1 GI:673074

LOCUS DEFINITION ACCESSION NID

RESULT

us-09-037-472-3.rst

KEYWORDS

JOURNAL

TITLE

FEATURES

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A1365968 430 bp mRNA EST 07-JAN-1999 a091006.X1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953226 3' similar to SW:HESI_RAT Q04666 TRANSCRIPTION FACTOR A1365968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 430)

11111er,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,C., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NOI human EST Project
Unpublished (1997)

On Jan 17, 1998 this sequence version replaced gi:2044405.
                                                                                                                                                                                                        Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
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This clone is available royalty-free through LNL; contact the
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This clone is available royalty-free through LNL; contact the
This clone is available royalty-free through LNL; contact the
This clone is available royalty-free through LNL; contact through 
Martin,J., Moore,B., Schellenberg,R., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
                                                                                    Unpublished (1997)
On Nov 29, 1993 this sequence version replaced gi:635188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 30;
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94.7%;
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                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches 18; Conservative
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AI365968/c
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/fev_stage="3 months old"
/dev_stage="3 months old"
/note="corpan: brain: Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female: dev_stage=3 months old;
Sisolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(df) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.S. Sin press" 1 others
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2898901.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone
IMAGE:649129 5', mRNA sequence.
AA214464
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases: 1 to 359)

Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome
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Eutheria; Primates; Catarrhin!; Hominidae; Homo.
1 (bases 1 to 429)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read
                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 21, 1992 this sequence version replaced gi:276086
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95277534
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/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.4; DB 21;
Pred. No. 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-25b04"
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AA214464.1 GI:1813283
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Matches 18; Conservative
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Length 429; Indels

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Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                       //note--Organ: Drain; Vector: pBluescript SK- (Stratagene); Site_1: EcoRI; Site_2: XhOI: Double-stranded cDNA was prepared from human meningioma using primer by consequent adaptor was used on the 5' end of the cDNA as follows: S-ATTCGCARGARGARAACTAGTCGTGAGT(18)-3'. An EcoRI went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. Tumor identification by consensus pathology. This library was constructed by Dr. Martin Schiller (Johns Hopkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T27501 516 bp mRNA EST 12-JUN-1996 EST27116 WATM1 Homo sapiens cDNA clone 27116 similar to close to nucleolin, gb|M60858|HUMNUCLEO, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9, Rue Jules Hetzel, Meudon Bellevue, 92190 France Tel: 33 1 45 07 52 87 Fax: 33 1 45 07 58 90 Email: bouillau@infobiogen.fr automatic cycle sequencing of PCR amplified insert open reading frame 2. 515.
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -4(UUP from Gibco.
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrii: Hominidae; Homo.

(bases 1 to 316)

Bouillaud.F.

Study of expressed sequences tags in adipose tissue 1994
Unpublished (1994)

On Sep 21, 1992 this sequence version replaced gi:279106.

Other.Esrs: overlap gbf706050/106050, human Esr03939.

Contact: Frederic Bouillaud

Centre de Recherche sur l'Endocrinologie moleculaire et le
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94.7%; Pred. No. 41;
tive 0; Mismatches 1;
                                                                                                                                         /organism-"Homo sapiens"
/db_xref="taxon:9606"
/map="1; /map="1; /clone="IMAGE:1953226"
/clone_lib="Schiller meningioma"
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/strain="caucasian"
                                                                                                                                                                                                                                             /sex-"female"
/tissue_type-"meningioma"
/dev_stage-"72 years"
/lab_host="SOLR"
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Best Local Similarity 94.7°
Matches 18; Conservative
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Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eukaryota, Metazoa; Catarrhini; Hominidae; Homo.

Eutheria Primates; Catarrhini; Hominidae; Homo.

Bult,C.J., Lee,N., Kirkness,E.F., Meinstock,K.G., Gocayne,J.D., White,O., Sutton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Rilmek,K.M., Kelley,J.C., Homo,J.L., I.M. Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., PelleyJ.J.M., Phillps,C.A., Ryder,S.E., Soctt,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Gollins,E.J., Dinke,D., Feng,P., Ferrie,A., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Haseltine,W.A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.S., Greene,J.M., Hudson,P., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fiabds,C., Fraser,C.M. and Venter,J.C.

Initial Assessment of Human Gene Diversity and Expression Patterns Based Uppn 83 Million Basepairs of cDNA Sequence
      /db_xrei- ......
/clone="27116"
/clone="1116"
/clone="15" White adipose
/clone="lb="warm1"
/note="vector: lambda gtl1; Site_1: EcoRI; White adipose
tissue, sub cutaneous, adult, female. Purification of
polyA mRNA first strand priming with random
oligonucleotides. Ligation of adaptors EcoRI/NotI, cloning
in EcoRI site of lambda gtl1."
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for clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfoetdb.tigr.org)
Seq primer: M13 Reverse.
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STG64297 Human White blood cells Homo sapiens cDNA 5' end similar
to None, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                  84.0%; Score 16.8; D
90.0%; Pred. No. 85;
tive 0; Mismatches
/db_xref-"taxon:9606"
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SOURCE
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                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                    AA265846 494 bp mRNA EST 20-MAR-1997 mz53d03.rl Barstead mouse pooled organs MPLRB4 Mus musculus CDNA clone IMAGE:717125 5' similar to qb:M19961 CYTOCHROME C OXIDASE POLYPEPTIDE WB PRECURSOR (HUMAN); qb:M77040 Mouse cytochrome coxidase Vb subunit gene, complete cds (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free througn LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further infommation.
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 494)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Barstead mouse pooled organs MPLRB4"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterstön,R.
The WashD'HHMI Mouse EST Project
Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:638332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                      ö
                                                                                                                                 Length 296;
                                                        2 others
                                                                                                                                                                      Indels
 /clone_lib="Human White blood cells"
/tissue_type="white blood cells"
/note="Organ: blood" 58 t 2 o
                                                                                                                                 DB 20;
                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 220.
Location/Qualifiers
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/dev_stage="7 day"
/lab_host="DH10B"
                                                                                                                                                                      0; Mismatches
                                                                                                                                                     Pred. No. 80;
                                                                                                                                 84.0%; Score 16.8; 90.0%; Pred. No. 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/map="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone-"IMAGE:717125"
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                                                                                                                                                                                                            1 TGGCATTGATCTGGTTCATC 20
                                                                                                                                                                                                                               113 TGGCATTGTTCTTGTTCATC 94
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Matches 18; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Sadams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nauyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Bednarik, D.P., Cao, L., Kunglun, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Rymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Prister, C.M., and Venter, J.C.,

Fraser, C.M., A.M., A.M., A.M., C.M., A.M., Fields, C.,

Fraser, C.M., A.M., A.M., A.M., C.M., A.M., Fields, C.,

Fraser, C.M., A.M., A.M., A.M., C.M., A.M., Fields, C.,

Fraser, C.M., A.M., A.M., A.M., C.M., A.M., Fields, C.,

Fraser, C.M., A.M., A.M., A.M., A.M., C
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                AA305985 443 bp mRNA EST 18-APR-1997
EST176975 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
eIF-3 pl10 subunit, mRNA sequence.
AA305985
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/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                         Gaps
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Other_ESTs: THC189756
Contact: Kerlavage, AR
                                                                                         ö
    Length 494;
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The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
71: 3018699056
Fax: 3018699423
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    DB 30;
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/db_xref="taxon:9606"
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Score 16.8; DE
Pred. No. 84;
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Matches 18; Conservative
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LOCUS

ACCESSION VERSION KEYWORDS SOURCE

AA581691/c

ð g ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

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Eukaryóta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="486 - leaf primordia cDNA library from Hake lab"
  A1600819 384 bp mRNA EST 21-APR-1999
486072c05.x1 486 - leaf primordia cDNA library from Hake lab Zea
mays cDNA, mRNA sequence.
A1600819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="leaf primordia"
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/dev_stage="P7-P11 leaf"
/dev_stage="P7-P11 leaf"
/note="Organ: shoot; Vector: Lambda zap; Hake lab CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALO45670 500 bp mRNA EST 30-APR-1995
DKFZp434A086_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434A086, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 500)

Koehrer, K., Beyer, A., Mewes, W., Gassenhuber, J. and Wiemann, S. EST (Koehrer, et al.)

Unpublished (1999)

On Jun 5, 1998 this sequence version replaced gi:3189015.
                                                                                                                                                                                                                                                                                                              Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
On Mar 20, 1998 this sequence version replaced gi:2979848.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
TTE: 650 723 2227
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Pred. No. 82;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: walbot@stanford.edu
Plate: 486072 row: C column
Location/Qualifiers
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AL045670.1 GI:4727868
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90.0%;
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Matches 18; Conservative
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                                                                                             ACCESSION
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RESULT
A1600819
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/lissue_type="kidney tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Corgan: kidney; Vector: Bluescript SK-; Site_1:
ECORI: Site_2: XhoI; Cloned unidirectionally. Primer:
Coligo dT. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATICGGCACGAG 3' 3' adaptor sequence: 5'
cTCGAGTTTTTTTTTTTTTTTTT 3' AVerage insert size: 1.0 kb."

a 60 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                  леритер 311 bp mRNA EST 26-SEP-1997
nn52a04.sl NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087470 3',
mRNA sequence.
AA581691
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 311)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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On May 5, 1995 this sequence version replaced gi:798355
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                Length 443;
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                                                        Indels
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;
                Score 16.8; DB 31;
Pred. No. 83;
                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 3325 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 289.
Location/Qualifiers
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90.0%; Pred. No. 80;
ive 0; Mismatches
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/clone_lib="NCI_CGAP_Kid6"
/sex="mixed"
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="3; 21"
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                                                                                               1 TGGCATTGATCTGGTTCATC 20
                                                                                                                     73 TGGCATTGTTCTTGTTCATC 54
                      84.0%;
90.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
                                                            Conservative
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                      Query Match
Best Local Similarity
Matches 18; Conserv
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Gaps

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source

FEATURES

BASE COUNT ORIGIN

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FEATURES

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Sebrafish.
Labor rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.

I (bases 1 to 451)

S Clark,M. Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Wasterston,R. and Wilson,R.
                                                         A1722423 451 bp mRNA EST 10-JUN-1999 fc27a12.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA 3' similar to TR:014777 014777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1998)
On Mar 10, 1998 this sequence version replaced gi:2949131.
Other_ESTS: fc27a12.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
W444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, U
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Possible reversed clone: similarity on wrong strand
Seq primer: T7 ET from Amersham
High quality sequence stop: 414.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xr=mum.__canto_relio
/db_xr=mum.__relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion_relion
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/lab_host~"XL1-blue MRF"
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94 c
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RESULT 12
AI72:433/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Betheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
Ottenwaelder, B., Obermaier, B., Mewes, W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                pSport1; Site_1: Not1; Site_2: Sall"
4 q 98 t 3 others
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81 c 115 g 79 t
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On Jun 5, 1998 this sequence version replaced gi:3189566
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MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany.
Location/Qualifiers
   Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany.
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/clone="DKRZp434(0319"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.0%; Score 16.8; DB 49; 90.0%; Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 49;
                                                                                                                                                                                                                                          /clone="DKF2p434A086"
/clone_lib="434 (synonym: htes3)"
/tssue_type="testis"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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90.0%; Pred. No. 84;
iive 0; Mismatches
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                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="14"
                                                                                               Location/Qualifiers
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452 TGGCATTGTTCTTGTTCATC 433
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AL049103.1 GI:4728413
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es 18; Conservative
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Best Local Similarity
Matches 18; Conserv
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AL049103/c
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KEYWORDS

SOURCE

VERSION

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FEATURES

COMMENT

Louis, MO 63108, USA

1 others

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Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="homo sapiens"
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/clone="Lib="434 (synonym: htes3). Vector pSport1; host
/dev_stage="adult"
/tissue_type="testis"
                                                                                                                                                                                                                                                                                                                                                                             Clone from S. Wiemann, sequenced by EMBL within the cDNA sequencing consortium of the German Genome Project sl sequence also available fris clone is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                    Ansorge W., Wirkner U., Mewes W., Gassenhuber J., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 708;
                                                                                                                                                                                                                                                                                                                                      Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases
MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 241 A; 135 C; 214 G; 118 T; 0 other;
                                                                                                                                        Homo sapiens mRNA; EST DKFZp434K122_rl (from clone DKFZp434K122)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens mRNA; EST DKFZp434G055_rl (from clone
DKFZp434G055)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.0%; Score 16.8; DB 54;
90.0%; Pred. No. 87;
iive 0; Mismatches 2;
                                                                                        12-MAR-1999 (Rel. 59, Created)
12-MAR-1999 (Rel. 59, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1999 (Rel. 59, Created)
12-MAR-1999 (Rel. 59, Last updated, Version 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 IGGCATIGITCTIGITCATC 149
                                                                                                                                                                                 EST; expressed sequence tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST; expressed sequence tag.
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                    Submitted (12-MAR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 708
                               AL044531.1
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HSM010310/c
ID HSM010310
   AL044531;
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                                                            e1402968
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/clone="DKFZp434M1522"
/clone=lib="434 (synonym: htes3). Vector pSportl; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone from S. Wiemann, sequenced by LMU within the cDNA sequencing consortium of the German Genome Project No SI sequence available the Sequence available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
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       DB 51; Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 53; Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
                                     Indels
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                                                                                                                                                                                                                                                                                                                                      Homo sapiens mRNA; EST DKFZp434M1522_r1 (from clone DKFZp434M1522)
                                    ;
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59, Last updated, Version 1)
 84.0%; Score 16.8; D
90.0%; Pred. No. 83;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.0%; Score 16.8; F
90.0%; Pred. No. 89;
iive 0; Mismatches
                                                                                                                                                   HSM007819/c
ID HSM007819 standard; RNA; EST; 867 BP.
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                                                                             266 TGGCATTGATCAGGCTCATC 247
                                                          1 TGGCATTGATCTGGTTCATC 20
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Matches 18; Conservative
                 Local Similarity
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12-MAR-1999 (Rel.
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Gaps

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Homo sapiens (human)
Eukaryöta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
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DH10B; sites Not1 + SalI"
/dev_stage="adult"
/tissue_type="testis"
                                                                                        Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
                                                                                                                                                                   Clone from S. Wiemann, sequenced by Qiagen within the cDNA sequencing consortium of the German Genome Project No s1 sequence available This clone is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                         Submitted (12-MAR-1999) to the EMBL/GenBank/DDBJ databases.
MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 539 BP; 190 A; 105 C; 163 G; 81 T; 0 other;
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                                                                                                                                                                                                                                                                                                                       source
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Search completed: September 18, 1999, 06:47:34 Job time: 3651 sec

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Query Match

Best Local Similarity 90.0%; Pred. No. 85;
Matches 18; Conservative 0; Mismatches 2; Indels 0

us-09-037-472-2.rge

Perfect score:

Run on:

Sequence:

Scoring table:

Searched: Database

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AC007066 Homo sapi
AC004705 Arabidops
AC005398 Arabidops
295152 Homo sapien
M25855 Human von W
                                                                  ACO06586 Home sapi
ACO06549 Home sapi
ACO06549 Home sapi
ACO07041 Home sapi
ACO07041 Home sapi
ACO07041 Home sapi
ACO07041 Home sapi
ACO07096 Archaeogl
272572 S.cerevisia
ACO07098 Archaeogl
ACO07098 Home sapi
ACO06982 Home sapi
ACO06981 Arabidops
278543 Caenorhabdi
ACO06687 Arabidops
ACO06687 Arabidops
ACO06687 Arabidops
ACO06687 Arabidops
ACO06981 Descritius
ACO06981 Descritius
ACO01438 Clostridi
ABO09003 Pyrococcu
X68367 M.thermofor
X68367 M.thermofor
ACO01438 Clostridi
ABO16081 Oryzias I
AEO33802 Tilapia m
AFO33802 Tilapia m
AFO33802 Tilapia m
ACO0688 Arabidops
ACO0688 Arabidops
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STS.name = Dm170B4
clone_name = 170B4
stS_from_promoter = T7
vector_class = cosnid, Lorist 6
origin_of_clone = Oregon-R
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Drosophila melanogaster

Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Perygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;

Drosophilidae; Drosophila.

1 (Dases I to 267)

European Drosophila Mapping, Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                     HUMVWFA28
AC003666
AC006576
AC006576
AC004046
AC07041
AE001062
SCYGL050W
ATAC003096
F15K9
HSU23143
                  ATAC004705
ATAC005398
HS179N16
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ATAC006282
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AC004982
AC004948
AC005748
AC005018
CNS00000
HS120G22
CELT01B11
CET20B1
AC00748
AC00748
AC006587
CEF20B
AC00648
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   VERSION
KEYWORDS
SOURCE
ORGANISM
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DM170B4T/C
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
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                                                                                                                       September 18, 1999, 15:48:25; Search time 436.05 Seconds
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                    GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                                                                                                                                  679419 segs, 1590154680 residues
                                                                                      OM nucleic - nucleic search, using sw model
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Match Length DB
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Direct Submission

Direct Submission

Submitted (O.2-AR-1999) Whitehead Institute/MIT Center for Genome Submitted (O.2-AR-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Mar 24, 1999 this sequence version replaced gi:4454611.

All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html.

Location/Qualifiers

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Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                      Genome
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2 (bases 1 to 190815)

Shiren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baker, J., Barlay, J., Calangelo, M., Ecchelly, R., Benn, J., Brown, A.,
Baker, J., Barlay, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,
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Raratas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P.,
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Maldrim, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J.,
Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,
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Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,
Wheeler, J., Wux, Wyman, D., Ye, W.J. and Zody, M.
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Homo sapiens chromosome 9, clone hRPK.355_0_1, complete sequence.
AC007066
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database_version = 45.0 and updates till date_of_search
date_of_search = 08-01.1996
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database_vearcion = 32.0
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.8; DB 14; Length 267; Pred. No. 20;
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                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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90.0%;
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Best Local Similarity 90.09
Matches 18; Conservative
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JOURNAL
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AUTHORS
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repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region	repeat_region	repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region	repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region

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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur-epm.ornl.gov), Genefinder (Phil Green, University of Mashington), Genscan (Chiris Burge, Inchiris Burge, Inchiris Chiris Burge, Inchiris Chiris Complete sequence against a peptide database and the Arabidopsis EST database at IIGR (http://www.tigr.org/tdb/at/at.html).

Annotated genes are named to indicate the level of evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e-mail: rounsley@tigr.org
BAC clone F26C24 is from Arabidopsis chromosome II and is near the
molecular marker mi398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 89840)
Rounsley,S.D., Kaul,S., Lin,X., Ketchum,K.A., Crosby,M.L.,
Brandon,K.C., Sykes,S.M., Mason,T.M., Kerlavage,A.R., Adams,M.D.,
Somerville,C.R. and Venter,J.C.
Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (24-JUN-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Jun 24, 1998 this sequence version replaced gi:3242697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (20-MAY-1998) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, rounsley@tigr.org 3 (bases 1 to 89840)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The orientation of the sequence is from SP6 to 17 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS ATACO04705 89840 bp DNA PLN 09-SEP-1998 DEFINITION Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence,
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                                                                                                                                                                                                                                                                                  DB 42; Length 190815; 34;
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                                                                                                                                                                                                                                                                             Query Match 80.0%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 34; Matches 16; Conservative 0; Mismatches
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The Institute for Genomic Research
9712 Medical Center Dr,
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Rounsley, S.D. and Lin, X.
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                                                                                                                                                                                                                                                                                                                                                                                                    Db 39469 CTTCCGAGTATACATT 39484
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ATAC004705/c
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complement(5528. .5822)
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5666. .5808
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10887. .10960
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complement(9300. 9424)
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complement(10195. 10236)
/rpt_family="AT_rich"
10536. 10617
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/rpt_family="AT_rich"
complement(12443...12481)
/rpt_family="AT_rich"
12807...12926
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complement(13587 . 13640)

/rpt_family="AT_rich"

complement(13649 . 13777)

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14034 . 14068
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complement(8429. 8488)
/rpt_family="AT_rich"
8531. 8563
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complement(6246. .6272)
/rpt_family="AT_rich"
6557. .6594
                                                                                                         excellent_shadowexon"
complement(5853. .5883)
/rpt_family="AT_rich"
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/213. .7230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(8011. .8138)
/rpt_family="(TAAA)n"
complement(8088. .8197)
/rpt_family="(TAAAA)n"
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complement(6779. .685
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rpt_family="(TAAA)n"
3019. .13073
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3131. .13254
              /rpt_family="AT_rich"
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their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://fp.genome.washington.edu/RW/RepeatMasker.html). Regions of genomic Sequence that are not annotated as genes but have predicted exons by GRAIL are annotated as misc features.
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//DLXTEE_" PID: 93252805"

/db_xref="PID: 93252805"

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GSRSPKTARPSPSPLGPLGKPOSLTTHNDESMSRAGNEDMEVSPEDGESPSW
GSRSPLTARSKARFSTYNGINRETCOSGSELPDWITLRARLEKKLEMEGI
KLSKSDGAMLLNRGLNAYMRRLIEPCLSLASOQKRAVSNVSMLDFHAAMEVNPRVLGEE
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5124. 5167
/note="exon predicted by xgrail, quality good_shadowexon"
complement(5337. 5427)
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Anote="exon predicted by xgrail, quality marginal"
complement(201. .223)

/note="exon predicted by xgrail, quality marginal"
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/note="axon predicted by xgrail, quality good"
complement(2023. .2062)
/complement(abs predicted by xgrail, quality good"
complement(2546. .2602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="predicted by genscan and genefinder"
complement(977, 1852)
/gene="F26C24.1"
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marginal_shadowexon"
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/rpt_family="(TAAAA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by xgrail, quality
                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="hypothetical protein"
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complement(<977. .>1852)
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complement(3870. .3893)
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4276. .4450
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/note="exon predicted excellent_shadowexon" complement(123. .188)
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716. 2739
rpt_family="AT_rich"
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Annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy/tRNAscan-SE). Simple repeats are
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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BAC clone T6B13 is from Arabidopsis chromosome II and is near the
molecular marker mi398.
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Submitted (30-OCT-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Oct 30, 1998 this sequence version replaced gi:3763911.
Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The orientation of the sequence is from SP6 to T7 end of the BAC
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Submission
Submitted (07-AUG-1998) The Institute for Genomic Research, 971
Medical Center Dr. Rockville, MD 20850, USA, rounsley@tigr.org
3 (bases 1 to 92524)
                                                                                                                                                                                                                                                                                                                                                                                        ATAC005398 92524 bp DNA PIN 30-OCT-1998 Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence. AC005398
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                                                                                                                         8; Length 89840;
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/note="exon predicted by xgrail, quality
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0; Mismatches
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9712 Medical Center Dr,
Rockville, MD 20850,
                     marginal_shadowexon"
complement(14070..14120)
/rpt_family="AT_rich"
                                                                                                                            Score 15.8;
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AC005398.1 GI:3810584
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                                                                                                                         Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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 (bases 1 to Rounsley, S.D.

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KDVVVENLRQLCVYKVANETGKPWWWDYYDFQIRCPMKEKKYRRECABSYIKSLGI
BSKKLDKCMODPDADLONPYLKEEQDAQVGKGSRGDYILTPTLVVNNRQYRGKLEKSA
VLKALCSGFEETTEATCLTTDVESNECLDNNGGGWDRSANITACKDTFRGRVCECP
TVDGVQFKGDGYSHCDFSGPGRCTINNGGCWHEERDGHAFSACVDKDSVKCECPFR
GDGTKKCEDINECKEKKACQCPECSCKNITWGSYECSCSGDLLYIRDHDTCISKTGAQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="PID:g3810586"
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GEKLKKAISGGDMVNLNLDWREAVPHPDDRVEYELWTNSNDECGVKCDMLMEFVKDFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="APS kinase, 3' partial"
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/product="APS kinase, 3' partial"
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/db_xref="CI: 3810585"
/db_xref="
identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted exons by GRAIL are annotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1944. .2045)
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/rpt_family="Arthrith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement join (2577. .2675,2804. .2913,3018. .3146, 3235. .3301,3382. .3464,3835. .3916,3981. .4057,4402.4559. .4628,4729. .4817,4895. .5587,5682. .5985)
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/note="exon predicted by xgrail, quality good"
complement(1544. .1608)
/note="exon predicted by xgrail, quality marginal"
complement(1726. .1758)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="vacuolar sorting receptor-like protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(<103. .784)
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/gene="T6B13.1"
/codon_start=1</pre>
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complement(join(<103. .252,337. .477,557. .784))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .16468
/note="overlap with BAC clone F26C24
                                                                                                                                                                                                                                                                                                                              1. .92524
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1904. .2022
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AL (DASES I TO 1/2010)

AL (DASES I TO 1/2010)

AL SUBMILSSION

Direct Submission

AL Submitted (02-APR-1998) Chromosome 6 Project Group

(http://wwwsanger.ac.uk/HGP/Chr6/) Sanger Centre, Hinxton,

Cambridgeshire, CB10 13A, UK. E-mail enquires:

humquery(Sanger.ac.uk Clone requests: clonerequest(sanger.ac.uk

On Apr 8, 1998 this sequence version replaced gi:2505919.

IMPORTANY: This sequence state compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variations annotated may not be found in the sequence submission

corres; anding to the overlapping clone as we submit sequences with

only a small overlap as described above.

This sequence was generated from part of bacterial clone contigs of

human chromosome 6 mapping group and loannis Ragoussis, Futther

information can be found at http://www.sanger.ac.uk/HGP/Chr6/ This

sequence has been finished according to sequence map criteria as

infollows. An attempt is made to resolve all sequencing problems,

such as compressions and repeats, but not necessarily within known

annotated human repeat sequence elements (e.g. Alu). Where the

feature key.
                                                                                                                                                                                                                                                                      Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CPG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The true left end of clone 179N16 is at 1 in this sequence. The true right end of clone 524E15 is at 690.

The true left end of clone 179N16 is at 172048.

The true left end of clone 179N16 is at 172048.

The true left end of clone 179N16 is at 172048.

Cancer Institute by the group of Pieter de Jong.

For further details see http://bacpac.med.buffalo.edu/.
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               295152.1 GI:3036773
HTG: CpG island; CSaids binding protein; CSBP2; MAPK; Mitogen
activated protein kinase; MXI2; P38; SAFK4; Stress activated
                                                                                                                                                                                                                                                      03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172048)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluJo repeat: matches 302. .62 of consensus;
incomplete repeat"
1714. .1954
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        5
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/note="match: STS AL020972"
        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI1"
     ö
                                                                                                             6080 TACCTTCCGAGAATATAT 6062
                                                                                                                                                                                                                                                172048 bp
                                                          2 TACCTICCGAGIATACATI
        Conservative
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  17;
                                                                                                                                                                                                                 HS179N16/c
LOCUS
DEFINITION
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TITLE
     Matches
                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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KEYWORDS
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12199. 12282,12422. 12498,12566. 12647,12995. 13077,
13170. 13236,13328. 13456,13617. 13726,13904. 14002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HDSAIGNFGIPQYGGSMAGTVVYPKENQKSCKEFSDFSISFKSQPGALPTFLLVDRGD
CFFALKVWNAQKAGASAVLVADNVDEPLITMDTPEEDVSSAKYIENITIPSALVTKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAQILEKGGFTQFRPHYITWYCPHAFTLS:QCKSQCINKGRYCAPDPEQDFSSGYDG
KDVVVENLRQLCVYKVANETGKPWVWPDYVTDFQIRCPMKEKKYNKDCAESVIKSLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSRKIDKCMGDPDADLDNPVLKEEQDAQVGKGTRGDVTILPTLVVNNRQYRGKLEKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLKALC SGFEESTEPAICLSTDMEINECLDNNGGCWODKSANITACKDTFRGKVCVCP
TYOGYRKENDOSY SHCEPSGPGKTITHNGGCWHEREDGHAFSACVDKDSWKGEPPEFK
GDGYKKCEDINECKEKACQCPECSCKNTWGSFECSGSGDLLYMRDHOTCISKTGSOV
KSAWAAVWLIMLSLGLAAAGAYLVYKYRLRQYMDSEIRAIMAQYMPLDSOPEVPHTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEKLKKAISGGDMVNLNLDWREAVPHPDDRVEYELWTNSNDECGVKCDMLMEFVKDFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MKQLLCYLPWLLLLSLVVSPFNEARFVVEKNSLSVTSPESIKGT
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/rpt_family="AT_rich"
complement(7371. .7519)
/note="exon predicted by xgrail, quality excellent"
complement(nin(<7571. .7686,8006. .8191,9280. .>9331))
/gene="fbl3.3"
/gene="fbl3.3"
/gene="fbl3.3"
                                                                                                                                                                                                                                                                                                                                                                                         Company 3.3"
/note="predicted by genscan"
/note="predicted by genscan"
complement(join(7571. .7686,8006. .8191,9280. .9331))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="vacuolar sorting receptor-like protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Jours-Tredicted by genscan and genefinder"
complement(14856. 15944)
/gene="TGB13.5"
/note="Mypothetical protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14649. .14675
/note="exon predicted by xgrail, quality
marginal_shadowexon"
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complement(<14856. .>15944)
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Pred. No. 47;
                                                                                                    complement (6732. 6761)
/rpt_family="AT_rich"
7056. 7088
/rpt_family="AT_rich"
Complement/life"
                                                     complement(6613. 6657)
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="AT_rich"
10403. .10430
5592. .5618
/rpt_family="(CAA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="T6B13.4"
10583. 14255
/gene="T6B13.4"
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10201. .10329
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89.5%;
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Anote-"MER2 repeat: matches 125. .209 of consensus"
Moote-"MER2 repeat: matches 279. .344 of consensus"
Mote-"MER2 repeat: matches 279. .344 of consensus"
Mote-"MER2 repeat: matches 3. .371 of consensus"
Mote-"13 copies of 2 mer 96 % conserved"
Mote-"13. .1989
Mote-"13. .3989
Mote-"14. .3989
Mote-"14.
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/note="Aluub repeat: matches 2. .302 of consensus"
6951. 7084
/note="FLMAC repeat: matches 1. .133 of consensus"
7621. 7941
/note="Limaches 5068. .5387 of consensus"
7809. .8170
/note="Limc2 repeat: matches 15. .384 of consensus"
8255. .8378
/note="MERZ repeat: matches 13. .136 of consensus"
8396. .8603
/note="MERZ repeat: matches 291. .82 of consensus"
/note="MERZ repeat: matches 291. .82 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .463 of consensus"
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/note-*MER11A repeat: matches 60. .738 of consensus"
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                                                                                                     2258. .2543
/note="LIMB6 repeat: matches 566. .874 of consensus"
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                                                                                                                                                                            2548. .2848
/note="AluSx repeat: matches 301. .1 of consensus" 2879. .3160
/note="AluSx repeat: matches 277. .2 of consensus; incomplete repeat"
1956. .2257
/note="AluJb repeat: matches 1. .302 of consensus'
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/note="FLAM_A repeat: matches 133. .4 of consen 15244. .15289
/note="13 copies of 2 mer 100 % conserved" 15674. .15853
/note="match: Z63849 CpG Island clone 91c11" 16341. .15670
/note="MLT2FA repeat: matches 33. .394 of conse 16823. .16969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  incomplete repeat"
8605. .8691
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74350. 744330

74555. 24834

760te="MIR repeat: matches 41. .123 of consensus"
24515. 24834

760te="AluSx repeat: matches 302. .1 of consensus"
24840. .25452

760te="LiMC2 repeat: matches 1065. .772 of consensus"
760te="LiMC2 repeat: matches 11. .302 of consensus"
760te="AluDb repeat: matches 11. .302 of consensus"
760te="MIREA repeat: matches 63. .189 of consensus"
760te="MIREA repeat: matches 1. .390 of consensus"
760te="MIREA septemble repeat: matches 1. .390 of consensus
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/db_xref="SPTREMBL:015264"
/translation="MSLIRKKGFYRQDVNKTAWELPKTYVSPTHVGSGAYGSVCSAID
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7782. .28781.29276. .29347,29456. .29570,29695. .29742,
30.78. .30207,30365. .30473,33547. .33605,34826. .34955,
35525. .35643)
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/ gene="SAPK4"
/ note="match: proteins 014739 015124"
/ codon_start="match: proteins 014739 015124"
/ codon_start="color="match: proteins of the color="color="match: proteins of the color="color="match: protein (Stress Activated Protein Kinase 4 (Mitogotein_id="CAB08438.1"
/ protein_id="CAB08438.1"
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/product="dJ178N16.1 (Stress Activated Protein Kinase 4
(Mitogen Activated Protein Kinase p38delta))"
complement(26546. .35905)
                                                          71977. .18027

/note="MrI2FA repeat: matches 400. .450 of consensus"

19217. .19333

/note="Mir repeat: matches 262. .117 of consensus"

19471. .19693

/note="AluJo repeat: matches 85. .301 of consensus;
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                                        .627 of consensus"
                                                                                                                                                                                                                                                                                   incomplete repeat."
21034. .21432
/note="MERIB repeat: matches 1. .337 of consensus."
21701. .22077
/note="match: ESTS R71395 R69756 AA587582 AA629092
21706. .21985
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22054. .2225
/note="AluJb repeat: matches 131. .301
incomplete repeat"
complement(22217. .22628)
17278. .17886
/note="MER11B repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: ESTs R50012 R70180"
24456. .24530
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Pred. No. 45;
0; Mismatches
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89.5%;
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Best Local Similarity 89.5
Matches 17; Conservative
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Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.
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Livermore X chromosome library"
/map="Xp22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The repeat regions shown were identified using RepeatMasker by
                                                    Direct Submission
Submitted (09-DEC-1997) Molecular and Human Genetics, Baylor
Collage of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 151750)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="Gs-551019, U199A7, U209F2"
/chromosome="X"
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complement(17159. 17374)
/rpt_family="LiMB7"
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complement(15364. 15659)
/rpt_family="AluJo"
complement(15836. 16099)
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complement(2773. .2863)
rpt_family="MER5B"
3472. .4871
/rpt_family="LIPA2"
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omplement/7=1
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1487. .11618
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1757. .11981
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2660. .12782
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complement(6989. .7
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2879. 13195
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                 2 (bases 1 to 151750)
Worley, K.C.
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11128. .1150
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                                                                                                     Coaquiation factor.

28 of 38
Human placenta, leukocyte, fetal liver and cell line EB19 DNA
Human placenta, leukocyte, fetal liver and cell line EB19 DNA
clones lambda [1,2,7.9,11], h[6,7,18], c[1,2,3,4,5,9,14,18] and
pWE[5,8,123].

SM Homo sapions
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Structure of toley, E.A., Westfield, L.A., Worrall, N.K.,
Structure of the gene for human von Willebrand factor

E 90062044.
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1 (Dases 1 to 151750)

Muzny, D., Arenson, A.D., Brundage, E., Carvelli, K., Chen, E., Chen, J., Di, W., Ding, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Jackson, L., Jin, S., Kampal, R., Karpathy, S., Leal, B., Li, Y., Liu, W., Logan, O., Lu, J., LY, Martinez, C., Oswal, G., Perez, L., Rashid, N.D., Lu, Y., Martinez, C., Oswal, G., Perez, L., Rashid, N.D., Vay, R., Savage, L., Scherer, S. S., Shen, H., Timms, K.M., Todd, J., Vo, Q., Worley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC003666 151750 bp DNA PRI 05-MAY-1998 NHORO SADJENS XQ2 BAC GS-551019 (Genome Systems Human BAC library) and cosmids U199A7 and U209F2 (Lawrence Livermore X chromosome cosmid library) containing part of human chloride channel 4 gene,
                                                                                                                                                                                                                                                                                                                                                                     Draft entry and computer-readable sequence for [1] kindly provided by J.E.Sadler, 30-JUN-1989.
Location/Qualifiers
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                     18-SEP-1997
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HUMAWWFA28 1022 bp DNA PRI
Human von Willebrand factor gene, exon 35.
M2585 M25716
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Pred. No. 68;
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AC003666 AC002358 AC002360 AC003017
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="12pter-p12"
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AC003666.1 GI:2992476
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491. .>1022
/gene="VWF"
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Best Local Similarity 89.5%;
Matches 17; Conservative
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/gene="VWF"
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270. .490
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36898. 37069
/standard_name="STS1-cSRL-31b6-uA/cSRL-31b6-u2, Chr.
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                                                                                                                                                     23332. .23445
/rpt_family="LIPA4"
23469. .2358
23469. .2358
/rpt_family="FLAM_A"
complement(25042. .25067)
/rpt_family="POUV_A"
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/rpt_family_mRER31A"
/rpt_family="MER31A"
/rpt_family="MIR"
28608. _28643
/rpt_family="(TAAAA)n"
/rpt_family="(TAAAA)n"
/rpt_family="AluJb"
/rpt_family="AluJb"
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db_xref="dbsTs:32826"
38436. .38566
/rpt_family="LlMA1"
$8597. .38795
/rpt_family="LlPB3"
complement(38769. .40304)
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complement(40626. .40905)
/rpt_family="LiPA12"
40904. .41028
/rpt_family="LiPB3"
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40309. .40609
                                                                                         "LIMB7"
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25264. .25431
/rpt f--
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/rpt_family="AT_rich"
34912. .35382
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/rpt_family="(GA)n"
32352. 32572
/rpt_family="MIR"
                                            /rpt_family="Limb7"
20670. .21171
complement(17421. .19544)
/rpt_family="L1M4"
                        complement(19654. .19760)
/rpt_family="L1MB7"
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58. .38089
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35405. 35701
/rpt_family="AluSg"
35707. 36176
36178. 38428
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/rpt_family="MLT1D"
31072. .311f.
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/rpt_family="(GGA)n"
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33332. .23445
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29312. 204
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Humanian Bukaroa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Prinates; Catarrhini; Hominidae; Homo.

Eltheria; Linton,L., Nusbaum,C., Lander,E., Allen,M., Anderson,M., Barter,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins;S., Collymore,A., Castle,A., Cerny,J., Colangelo,M., Collins;S., Collymore,A., Castle,A., Cerny,J., Colangelo,M., Collins;S., Collymore,A., Castle,A., Cerny,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Herena,L., Horton,L., Howland,J.C., Jones,C., Kann,L., Karatas,A., Lehoczky,J., Macdonald,P., Marquis,M., Morris,W., Morrow,J., Morchan,K., Meldrim,J., Molla,M., Morris,W., Morrow,J., Pavlin,B., Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Subramanian,A., Tesfaye,S., Torruella-Miller,I., Vassiliev,H.,
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Homo sapiens chromosome 18, clone hRPK.430_E_17, complete sequence.
AC006249
AC0062902
AC006249.1 GI:4062902
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TITLE Direct Submission JOURNAL Submitted (12-DEC-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 10 197082) REFERENCE 1 (Dases 1 to 197082) AUTHORS Barren, Barna, N., Beckerly, R., Benn, J., Brown, A., Scatle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Deprive, E., Devon, K., Dewar, K., Donelan, L., Ferreita, P., Fitzhaldh, W., Forrest, C., Funke, R., Garge, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Herena, L., Horton, L., Howlind J.C., Jones, C., Kann, L., Karatas, A., Herena, L., Horton, L., Howlind J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Maddonald, P., Marghis, N., Mochan, P., McGurk, A., McKernan, K., Meldrim, J., Mollar, M., Morris, W., Morts, M., Mornan, D., Roberts, D., Ray, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella Miller, I., Vassiliev, H., Vo, A., Wanner, A., Wheeler, J., Wall, W., W., Wanner, D., Ye, W. J., and Zody, M.	TITLE Direct Submission JOURNAL Submitted (25-DEC-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA COMMENT On Dec 25, 1998 this sequence version replaced gi:4049322. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) Hith://fth genome usehinten additional Massers ham)	source 1197082  / .197082 // .197082 // .197082 // .197082 // .197082 // .2000="hRPK.430_E_17" // .2000="hRPK.430_E_17" // .2000="hRPK.430_E_17" // .256 // .256 // .256 // .256 // .256 // .256 // .2641 // .2	repeat_region complement(1135211bb9)  repeat_region 1168011701  repeat_region 170212290  repeat_region 7rpt_family="LIME3"  repeat_region 7rpt_family="LIME3"  repeat_region 7rpt_family="LIME3"  repeat_region complement(1243412607)  /rpt_family="MiR"  repeat_region complement(1271913059)

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Primates; Catarrhini; Hominidae; Homo.

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Homo sapiens chromosome 4, WORKING DRAFT SEQUENCE, 10 unordered
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s: gap of unknown length
s: contig of 1204 bp in length
s: gap of unknown length
s: contig of 3061 bp in length
s: gap of unknown length
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s: gap of unknown length
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gap of unknown length
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gap of unknown length
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AC004046.1 GI:3135247
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Submitted (14-MAY-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On May 14, 1999 this sequence version replaced gi:4803972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)

( the Cantu, L.A., McDermid, H.E., Simon, M.I. and Roe, B.A.

Cantu, L.A., McDermid, H.E., Simon, M.I. and Roe, B.A.

Direct Submission

Submitted (16-FBB-1999) Department Of Chemistry And Biochemistry,

The University Of Oklahom... 620 Parrington Oval, Room 208, Norman,

OK 73019, USA
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1 (bases 1 to 11684).

Cantu, L.A. and Roe, B.A.
Homo sapiens Chromosome 22q11.2 BAC Clone 762c12 In CES Region Unpublished (1997).
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DEFINITION * Homo sapiens Chromosome 22q11.2 BAC Clone 762c12 In CES Region,
complete sequence.
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Cantu, L.A., McDermid, H.E., Simon, M.I. and Roe, B.A.
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Klenk, H. B., Clayton, R. A. Tomb, J., White, O., Nelson, K. E., Katchum, K. A., Dodson, R. J., Gwinn, M., Hickey, E.K., Peterson, J. D., Ketchum, K. A., Dodson, R. J., Gwinn, M., Hickey, E.K., Peterson, J. D., Richardson, D. L., Kerlavage, A.R., Graham, D. E., Kyrpides, N. C., Fleischmann, R. D., Quackenbush, J., Lee, N. H., Sutton, G., Gill, S., Kirkness, E.F., Dougherty, B.A., McKenney, K., Adams, M. D., Loftus, B., Peterson, S., Reich, C. I., McNeil, L.K., Badger, J. H., Glodek, A., Interback, T., Cotton, M. D., Spriggs, T., Artiach, P., Kaine, B.P., Sykes, S. M., Sadow, P. W., D'Andrea, K. P., Bowman, C., Fujil, C., Garland, S. A., Mason, T. M., Olsen, G.J., Fraser, C. M., Smith, H. O., Woese, C. R. and Venter, J. C.

Direct Submission

AL Submitted (15-DEC-1997) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA

In order to show the genes in ascending order on the genome, the origin of this version has been moved by TIGR to position 2093570

of the original version and the opposite strand is shown from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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/transl_teable=11
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                                                                                                                                          Alcohardylous.

I (bases 1 to 10312)

Klenk,H.P., Clayton,R.A., Tomb,J., White,O., Ne. *>n,K.E.,
Ketchum,K.A., Dodson,R.J., Gwinn,M., Hickey,E.K., Peterson,J.D.,
Richardson,D.L., Kerlavage,A.R., Graham,D.E., Kyrpides,N.C.,
Fleischmann,R.D., Quackenbush,J., Lee,N.H., Sutton,G., Gill,S.,
Kirkness,E.F., Dougherty,B.A., McKenney,K., Adams,M.D., Loftus,B.,
Peterson,S., Reich,C.I., McNeil,L.K., Badger,J.H., Glodek,A.,
Zhou,L., Overbeek,R., Gocayne,J.D., Weidman,J.F., McDonald,L.,
Utterback,T., Cotton,M.D., Spriggs,T., Artiach,P., Kaine,B.P.,
Sykes,S.M., Sadow,P.W., D'Andrea,K.P., Bowman,C., Fujii,C.,
Garland,S.A., Mason,T.M., Olsen,G.J., Fraser,C.M., Smith,H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(254. .481)
/gene="AF0510"
/note="hypothetical protein; identified by GeneMark;
                                                                              Archaeoglobus fulgidus
Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               original version.
On Dec 16, 1997 this sequence version replaced gi:2649999.
Location/Qualifiers
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The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus
Nature 390 (6658), 364-370 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"conserved hypothetical protein"
Protein_id="Anab90626.1"
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identified
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complement(254. .481)
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/gene="AF0611"
         AE001062.1 GI:2689385
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                                                        SOURCE
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Submitted (06-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 5, 1999 this sequence version replaced gi:4371304.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* Tuns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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Homo sapiens clone NH0327N17, WORKING DRAFT SEQUENCE, 2 unordered
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173422)
Waterston, R.H.
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                             1717 others
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Pred. No. 75;
0; Mismatches
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/chromosome="4"
1 24409 c 23279 g 37501
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35597 c 34493 q
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AC007041.2 GI:5001509
HTG; HTGS_PHASE1.
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Waterston, R.H.
                                                                                                                      77.0%;
94.1%;
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94.18;
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Best Local Similarity
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CDS

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NYVKDYKKLVDMPEKPYKFAVTLEIAVEDSNKVPGWEELKKRLSKFFYERGFGGAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MFVNGTPVIEIVLSNPLLSVKFPESGSVLAVIDTGYEGFAVVPQ
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LGTEFLEGFKLVGTRSFEISSCW"
complement(2055..2372)
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/note="hypothetical protein; identified by GeneMark;
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complement(2718. .2999)
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complement(3104. .3493)
                                                                                                                                       complement(1679. .2065)
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gene

CDS

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LIYILITLENKUPRYIMPUDFVALSIGVEVSSLANRKYSTILTEILLFGLLNISA
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complement(5115. .6191)
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DFRNIKSSVLGIVFGIPGIAELTKWNARVYIIPSIFALCLVNYPHRCPYCHQIVKNGWKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MEKNLYDTNKLIELYKNKESMSGYTTILNVIEFPKALEFNLTVL
YLSKSDYRLAIKISTELLKIGEPVPAVYTLISAIANKQRFKGCNAGQTFYAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to GB:L77117 PID:1500505 percent identity:
29.04; identified by sequence similarity; putative"
/codon_start=1
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Saccharomyces cerevisiae
Eukaryota; Fungil, Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 2468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="AF0618"
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S.cerevisiae chromosome VII reading frame ORF YGL050W.
272572 Y13135
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85.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                        complement(5115. .6191)
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/gene-"AF0619"
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                                                                                                                                                                                                                                                                                                                                                      /gene="AF0617"
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17; Conserv
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Best Local
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SCYGL050W/c
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prediction programs including GRAIL (available by anonymous ftp from arthur.epm.orn.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/netpgene./cbsnetpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypotherical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Chankascan-SE). Simple repeats are hittp://denome.wustl.adv/eddy/tRNAscan-SE). Simple repeats are hittp://denome.wustl.adv/eddy/tRNAscan-SE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(<1. .273,386. .516,635. .1947,2188. .>3330))
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EETKLLQDOAGSREKEINELRDLKKETLRADSSEERRHARFELNKAKALIVKDEEI
EOD PEVKREISLVKNLLASERQKTESEEKKKABKKKADKYLSELEVLKNSAHKTSS
DLLTITSNLETVKKQLELEKOKTLKEKKRADKSSARADOMKLAEDVSKKFEIVBARN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e-mail: rounsley@tigr.org
BAC clone T29F13 is from Arabidopsis chromosome II and is near the
molecular marker ve016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1. .1207)
/gene="T29F13.1"
/note="overlap with BAC clone F1913 (AC004238:1. .1207)"
                                                                                                                                                                                                                                                                                       Submitted (13-MAY-1998) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On May 13, 1998 this sequence version replaced 91:3126888. Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                Submitted (07-NOV-1997) The Institute for Genomic Research, 971 Medical Center Dr, Rockville, MD 20850, USA, rounsley@tigr.org Rounsley,S.D.
Somerville, C.R. and Venter, J.C.
Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence
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/organism="Arabidopsis thaliana"
/cultivar="Columbia"
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/clone-"T29F13"
                                                                           2 (bases 1 to 69817)
Rounsley, S.D. and Lin, X.
Direct Submission
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                                                                        to 69817)
                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                      Steve Rounsley
                                                       Unpublished
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AUTHORS
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SADMYTTSSCSGRVSVFLEGTKSYNGEVKIGGKGGGKWLYVTHDREKVIGNLDELKS
SKEFEFELSCKEIPPEKVTGSIRYILKKYEPFILHVKCRPQAASKLYNTAMSCGFRE
SGIGSNNLVAIRNIKLDVPLGYLDETSGTLKFFVTPEYVSVLDSLSKEREDRTRKM
QALVDRIEKELINCAPDVNSKVNITPTETKEERREKKREGMERQRQLKSPQNVL*
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Rounsley,S.D., Lin,X., Ketchum,K.A., Crosby,M.L., Brandon,R.C.,
Sykes,S.M., Kaul,S., Mason,T.M., Kerlavage,A.R., Adams,M.D.,
                              Direct Submission
Submitted (14 MAY-1996) Data collected by MIPS on behalf of the European yeast chromosome VI sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; E-mail: Mewes@mips.embnet.org 2 (bases 1 to 2468)
Feuermann,M., de Montigny,J., Potier,S. and Souciet,J.L. The characterization of two new clusters of duplicated genes suggests a 'Lego' organization of the yeast Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATACO03096 69817 bp DNA PLN 25-SEP-1998
Arabidopsis thallana chromosome II BAC T29F13 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="tR(TCT)GL - systematic name"
/note="tR(TCT)GL - common name; anticodon gene: TCT"
1079. .1150
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/db_xref="taxon:4932"
/chromosome="VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1079. 1150 ----- common name: ant /gene="tR(TCT)GL - systematic name" 1385. 2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA96752.1"
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/db_xref="PID:g1325543"
/db_xref="GI:1322543"
/db_xref="SHISS-PROT:P53177"
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/note="delta-remnant"
complement(837. .1062
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1079. .1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="delta-remnant"
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/note="ORF YGL050w"
                                                                                                                                                                                                                                                              cerevisiae chromosomes
Yeast 13 (9), 861-869 (1997)
97377993
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AC003096
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      1. .2468
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                                    TITLE
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FEATURES
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     AUTHORS
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KKULPIGERKETIONNINGERFEETUVPPDROGGSSADDITVSKERVENKER

KKULPIGERKETLOSMINGERSEPSEKEETUVPPDROGGSSADDITVSKERVENKEK

IIVONSLEFNGSGRFPGULAGKTTCLSTATGHDVKTLESDDAATDYWKLLELDNLEE

ENYYOMARSILSPDLPQVDFLGCEIMNEDNPARAIDLAASNSWYLRFILESSESS

LNTONISVTVEMPPHIKPLEGELKHITIVFSNYHTTRTGNTLNVDSFSCLDSF

SKHIRGVADTLESLKMEDNLAQERACVFLSLLIHNFSWYHTTRTGNTLNVDSFSCLDSF

SKHIRGVADTEAGVALSGFSEELCLLQDLLSGQRVLFSVKSSETCESDLSIPVTLN

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284. 368

"Tpt_family="(TAAAA)"

complement(3421. 3496)

/note="exon predicted by xgrail, quality excellent"

complement(3822. 3374)
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TGCRKLLTLNGVRNRNGEKKBDARCLYSGYQEQACKLSAHLISKSGRGVESVSG
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TISQLESPTGGSRKNENGLENGVROULLASQGREQFSVTTSAETAKDRNIQP
TKSSMLQKISDTSKNGNLCLVAENYLQRCQRDIHENSRKRKRMLEAVVSHKHLASGDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MVAQGFTVDLKKPLVFQVGHLGEDYEEWVHQPIATKEGPRFFQS
DFWEFLTLTVWWAVPVIWLPVVVWCISRSVSMGCSLPEIVPIVVMGIFIWTFFEYVLH
RFVFHIKTKSYWGNTAHYLIHGCHHKHPMDHLRLVFPPTATAILCFPFWNIAKAISTP
STAPALFGGGMLGYYMYDVTHYYLHHAQPTRPVTKNLKKYHLNHHFRIQDKGFGITSS
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8304. 8395
/note="exon predicted by xgrail, quality good"
/inote="exon predicted by xgrail, quality good"
join(8739. 9741,9833. 9979,10031. 10135,10253. 10378,
10487. 10555,10667. 10788,11071. 11158,11340. 11453,
/gene="T29F13.4"
/gene="T29F13.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(8739. 8867,8989. .9078,9171. .9242,9347. .9418,
9505. .9741,9833. .9979,10031. .10135,10253. .10378,
10487. .10555,10667. .10788,11071. .11158,11340. .11453,
79ene="T29F13.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="FAH1; identical to GB:AF021804"
complement(join(4470 .4589,4692 .4838,4916 .5021,
5155 .5351,5460 .5552,5705 .5755))
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWDIVEGILPTIKAPRKEQ"

6909. .6963

7004e-"exon predicted by xgrail, quality marginal"

7298. .7366

7004e-"exon predicted by xgrail, quality excellent"

77682. .77862

79ene-"T29F13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     excellent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(4301. .4589,4692. .4838,4916. .502
5155. .5351,5460. .5552,5705. .5770,6641. .6864))
/gene="T29F13.2"
complement(4301. .6864)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="exon predicted by xgrail, quality 3824. 3909
/note="exon predicted by xgrail, quality carellers, shadowexon" 4003. 4101
/note="exon predicted by xgrail, quality marginal_shadowexon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="fatty acid hydroxylase, FAH1"
/protein_id="AAC167")0.1
/db_xref="PID:93132481"
/db_xref="R133481"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="tubulin pseudogene"
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/db_xref="PID:93132470"
/db_xref="GI:3132470"
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gene

CDS

mRNA

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/translation-"MEDFIVADTRTVKGHNLGLYAIFDGHSGSDVADYLQNHLFDNIL
SCAPEPWRNPRKAIKRAYKSTDDYILQNVVGPRGGSTAVTAIVIDGKKIVVANVGDSRA
ILCRESDVVKQITVDHEPDENELVKSKGGFVSQKPGNVPRVDGIAMTRAFGDGGLK
EHISVIPNIETAEIHDDTKFILLASDGLMKVMSNDEVWDQIKKRGNAEEAARMLIDKA
LARGSKDDISCYVVSFLQMID"
/translation="MGAVELMSDPSSLCTVENYVDNVDLSDTQLVQTVRKALTSVKTG
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Arabidopsis thaliana

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="exon predicted by xgrail, quality good_shadowexon" complement(13470. .13517)
/note="exon predicted by xgrail, quality excellent" complement(13619. .13684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 71097)
Vysotskaia,V.S., Schwartz,J.R., Toriumi,M., Yu,G., Li,J., Liu,S., Kremenetskaia,V.S., Schwartz,J.R., Araujo,R., Buehler,E., Conway,A.B., Dewer,K., Feng,J., Kin,C., Li,Y., Shinn,P., Sun,H., Davis,R.W., Ecker,J.R., Federspiel,N.A. and Theologis,A.
Unpublished (1998)

2 (bases 1 to 71097)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F15K9 71097 bp DNA PLN 07-NOV-1998
Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%; Score 15.2; DB 8;
85.0%; Pred. No. 1.1e+02;
Live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="(CAT)n"
13247. .13362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 49061 GGAACCTCCGAGTATACATT 49080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13246. .13359
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AC005278
93789706
AC005278.1 GI:3789706
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Best Local Similarity 85.09
Matches 17; Conservative
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Direct Submission

gene

CDS

mRNA

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// protein_id="aAc72108.1"
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// db_xref="gi:3850568"
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FOHDOSLOLQARSQYGKLEKGQLLKVDPYLVRRSKHHFHYVESLGIDLIIGCNGFIW
VGEHVEVRDPMAIDDOKDEEMISSSSTGKEOSHIPLETROTICRIGNAIRUSNIGFT
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| Maxaref="PiD::q3850366"
| Ab_xref="G1::B350366"
| Ab_xref="G1::B350366"
| Atranslation="MSIVOKOEEMNGCGLNVDKVEAFTVSPQEKGRKNKRKLADPSOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NASSLIEFPPYELPSLKPQNHLSGNGSVGEVSNQLQVEVSEŠVEMDDPFACHLEELLS
SNLLTLFLDTMKQLIDLGYTDDEVLKAVSRCRLYCGGNNLLSNIVNNTLSALKT<br/>\text{DEG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGSGDYVFEDLQQLVSYTLVEMISLIKEVRPSLSTVEAMMRLLMCDLNVLQAFEA. GD
GLYSSKRLSDSESLGAESNRPKSSDPDNRPRPOSDSQBQSNRNEPLKFGNRPNTPNSKKT
GSGGTTPGKEVCSGGTVSCQGMRSTSFTLVSDEKLVSCRKGRTKKEIAMIRQKSCVEK
IRTYSKGSGYKAAKFASVGSFLLEKRVKSSSEFVPRNSSSKITAEIGVRYSLAEDSGG
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/translation="WNFFKSVFTEDLDPPFTESESDSPKHSEEHEHPEQEHPEQSESN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOGGWSFGGLMKTLATRSESVIETYRRDLEEFGTGLKKEIEVAQGSLGTVGHAIDELG
NTVLKGTAEIIAQGKEAILAAGNESDSSDNNSSQSFGRRDSFSSKPYSRFDAQIRAVQ
GDLNTYCEEPEDSDDYKKWESAFSLDGKAEEMEKLLEENGDMKGVYKRVVPSWYDHET
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EKKETDSEEVPEEKSFVDAAPPASDEAPIQDSVKPTSDEAPIQDSVKPKSDEAAPSQD
SAKPDVAASSSTQQPSEEDLGWDEIEDMSSIDGKETSRSGGSPNRAELRKRLSAAEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(10217. .10651,10741. .10809,10909. .10974, 11054. .11143,11249. .11294,11404. .11505,11583. .11743))
//gene="F15K9-4"
//note="F15K9-4"
//note="F15K9-4"
//note="Similar to hypothetical protein SPAC2F7.14c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FWFRYFYRVNKLKQAEDLRANLVKRAISLDDEEELSWDIDDEEESSEKVVEATKDVSR
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16319. .16499,16613. .16684))
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/gene="F15K9.5"
12150. .13562
/gene="F15K9.5"
/gene="F15K9.5"
/note="ESTS gb|T21276, gb|T45403, and gb|AA586113 come
from this gene."
                                                                                          (join(6205. .6675,7214. .9214))
K9.3*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGMMDCPSCRGTIHRRIQARFARSG"
complement(10217. .11743)
/gene="F15K9.4"
                                                                                                                                                                                                             /evidence=not_experimental
/product="F15K9.3"
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2826. .2942,3029. .3312,3461. .3643,3756. .4976,5083. .5428))
/gene="Fl5K9.2"
                                                                                                                                                                                                                                                                                                                                                                                                                              St., Albany, CA 94710, Used to the Lypession center, but Buchanan on oct 24, 1998 this sequence version replaced gi:3406036.

This sequence is of BAC F15K9 from Arabidopsis thaliana chromosome in the sequence does not represent the sequence of the entire insert of this clone. It is shorter by 26,439 bp because we submit only the unique sequence of the clone. In order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide a small overlap (200 bp) between overlapping submitted clones. The 5' end of this sequence overlaps by 200 bp the 3' end of the sequence of BAC F21B7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Contains similarity to gb|AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF|00168. ESTS gb|AA585988 and gb|T04384 come from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MMKKGKGKNSGLLPNSFKIISSCLKTVSANATNVASSVRSAGAS
VAASISAAEDDKDQVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFLWEDIEEIQVLPPTLASMGSPIVVMTLRPNRGLDARIGAKTHDEEGRLKFHFHSFV
SFNVAOKTIMALWKAKSLTPEOKVQAVEEESEGKLQSEESGLFLGVDDVRFSEVFSLT
LPVPVSFFMELFGGGEVDRKAMERAGCOSYSCSPWESEKDDVYERQTYYRDKRISRYR
GEVTSTQOKSLVPEKNGWLVEEVMTLHGVPLGDYFNLHLRYQMEESTSKPKTTYVRVY
Submitted (11-JUL-1998) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA (bases 1 to 71097)
                                                                                                                                                                                            Submitted (24-OCT-1998) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA 4 (bases 1 to 71097)
                                                                                                                                                                                                                                                                                                                   Theologis.
Direct Submission
Submitted (07-NOV-1998) Plant Gene Expression Center, 800 Buchanan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note "This gene is cut off; it is continued from BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGIEWLKSTRHOKRVTKNILVNLQDRLKMTFGFLEKEYSSROOQQQVT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/protein_id="AAC72107.1"
/db_xref="PID:g3850567"
/db_xref="G1:3850567"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3702"
/chromosome="1"
/clone="f15K9"
complement(59. 241)
/gene="F15K9.1"
/gene="F15K9.1"
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                                                                                                                                                                Direct Submission
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                                                                                                                  Theologis, A.
                                                                                                                  AUTHORS
TITLE
    JOURNAL
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                                                                                                                                                                                                JOURNAL
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                                                                             REFERENCE
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 18, 1999, 05:27:13 ; Search time 213.04 Seconds Run on:

(without alignments)
23.488 Million cell updates/sec

US-09-037-472-2 20 1 GTACCTTCCGAGTATACATT 20

Perfect score: Sequence:

IDENTITY\_NUC Scoring table: 311585 segs, 125096042 residues Searched:

N\_Geneseq\_36:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		ukin-	n 7-transmem	cDNA encoding a hu	Tumour rejection a	Aspergillus niger	Continuation (8 of	EST clone D1160. N	Staphylococcus aur	Enterococcus faeca	Mouse metastasis-a	6	6	Transforming growt	ь	Transforming growt	ה	ה	ь	6	5			Guinea pig MBP-1 g	Наето	Mouse LTBP-3 gene.	o	ß	DNA molecule encod	Nucleotide sequenc	ns	ß	υ		Clostridium chauvo		Clone contg. hom-t	odingse	w		ice of e		Sequence encoding	Encodes T lymphocy
COLUMNIA	ID	•	35	V62388	V71117	T11549	V28496	V21209_07		V74403		V12500	T65154	T65155	T65156	T65157	T65158	T65159	T65160	T65161	T65162	T65166	T65169	X13508	Q31988	078916	099863	T47220	V43042	V68924	V68233	V74506	x13205	X13058	X13772	X00225	040491	N81712	N81774	N70543	006827	N70951	012118	609	021184
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	9	1	20	1578		13585	2436	110000	278	6022	5069	5137	125	125	125	116	123	117	123	115	116	116	78	5621	897	1720	3756	1193	7715	289	CA.	13715	2311	8033	1076	1560	885	3685	877	12492	4839	997	2259	2615	2350
ď	Query Match	!	$\overline{}$	$\sim$	$\sim$		_	_	_	~	-	$\circ$	$\boldsymbol{\sigma}$	O.	an.	on.	ത	an.	ത	O.	on	ത	on.	o	œ.	œ	œ	œ	œ	œ	œ	œ	œ	œ	œ	w	~	w	Ψ	w	Ψ	w	0.99	w	w
	õ		20	₹.	4	14.2	4	4	4	14.2	4	_										13.8				13.6		13.6							13.6								13.2		
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complify the IL-1-alpha (IL-1-alpha) primers 2 and 1 (V12389) were used to amplify the IL-1-alpha gene region to identify single base variation of polymorphism of c/T at base 889. The invention claims to provide a method for predicting the risk of sight threatening diabetic retinopathy. The method involves isolating DNA from a patient and determining the DNA polymorphism pattern of the genes that code for interleukin-1-alpha, interleukin-1-beta and interleukin-1RN. The polymorphic pattern interleukin-1-beta and interleukin-1RN. The polymorphism patterns thereby identifying patients carrying a genetic polymorphism patterns thereby identifying patients carrying a genetic polymorphism sosociated with increased risk of sight threatening diabetic retinopathy. The method may be able to identify diabetic patients at risk before the clinically detectable disorders occur. Polymorphism pattern clinically detectable disorders occur. Polymorphism pattern (V12398). The method is also claimed to be useful in conjunction with retinopathy in genesi navolved PCR reactions using primers V32389. Continued to the useful in conjunction with retinopathy in genomic DNA and therefore, in identifying diabetic patients expressing multiple risk patterns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 7-transmembrane receptor polypeptide, HWTMF81 encoding cDNA. MWTMF81, 7-transmembrane receptor; treatment; infection; bacteria; pain; fungal; protozoan; viral; human immune deficiency virus; HIV-1; HIV-2; cancer; anorexia; bullmia; asthma; Parkinson's disease; heart failure; hypotension; hypotension; hypotension; hypotension; vinary retention; osteoporosis; allergy; angina pectoris; myocardial infarction; asthma; allergy; ulcer; anxiety; prostatic hypertrophy; psychotic disorder; neurological disorder; human;
Encodes T lymphocy
                      Human Leu8 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RENN/) RENNIE I.

(RICH/) RICHARDSON R.

Duff G, Rennie I. Richardson R;

WPI; 98-240835/21.

Preddicting increased risk of sight-threatening diabetic retinopathy - comprises identifying genetic polymorphism pattern for genes IL-1R, IL-1B and IL-1RN, useful to allow treatment before clinical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                11-SEP-1998 (first entry)
Interleukin-1-alpha primer 2 (-888/-869).
IL-1-alpha; qenetic polymorphism; PCR; primer; amplification;
sight threatening diabetic retinopathy; interleukin-1-alpha;
interleukin-1-beta; interleukin-1RN; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 20; DB 1; Length 20; 100.0%; Pred. No. 0.025; tive 0; Mismatches 0; Indels
                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 33; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V62388 standard; cDNA; 1578 BP.
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                                                                                                                                                                                             V32390 standard; DNA; 20 BP
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  1914
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09-OCT-1997; G02790.
10-OCT-1996; GB-021129.
(DUFF/) DUFF G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
  66.0
66.0
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WO9815653-A1.
13.2
                                                                                                                                                                                                                                                                                                                                             Synthetic.
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V62388
  44
                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The HYMPREI polypeptides and polynuclectides can be used in the treatment of infections such as bacterial, fungal, protozoan and viral infections. They can be used particularly for treatment of infections caused by the bacterial bulbinata asthma. Parkinson's disease, acute heart failure, hypotensia, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma, allergies, benign prostatic and neurological discorders, including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's disease or
                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding 7-trans-membrane receptor polypeptide HWTMF81 - useful in treatment of e.g. infections such as bacterial, fungal, protozoan and viral infections, particularly HIV, cancers and bulimia etc. Claim 5, Pages 7-8; 22pp; English.

This cDNA encodes a human 7-transmembrane receptor polypeptide, HMTMF81.
schizophrenia; manic depression; delirium; dementia; mental retardation;
dyskinesias; Huntington's disease; Gilles dela Tourett's syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSTEB-1999 (first entry)

OSTEB-1999 (first entry)

Human; 7-transmembrane receptor designated HMTMF81.

Human; 7-transmembrane receptor protein; HMTMF81; infection;

HIV; pain; cancer; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; asthma; benign prostatic hypertrophy; neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding 7-transmembrane receptor polypeptide HMTMF81 - useful for treatment of, e.g. HIV infections, pain, cancers, myocardial infarction and acute heart failure
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                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Ames R, Chambers J, Ellis C, Foley J, Halsey W,
                                                                                                                                     /product= "HMTMF81 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.0%; Score 14.4; 193.8%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product- HMTMF81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-1997; 308560.
22-ART-1997; US-844795.
(SMIK ) SMITHKLINE BEECHAM CORP.
Ellis CE, Halsey WS, Sathe GM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gilles dela Tourett's syndrome.
Sequence 1578 BP; 480 A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V71117 standard; cDNA; 1578 BP.
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/*tag= a
                                                                                          . .1480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.0
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 CCTTCCGAGTATACAT 19
                                                                                                             /*tag=
                                                                                                                                                                                                      20-APR-1998; 303008.
19-MAR-1998; US-844795.
22-APR-1997; US-844795.
                                                                                                                                                                                                                                                                                                                                         Sarau H, Sathe G;
WPI; 98-544641/47.
P-PSDB; W75799.
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18-NOV-1998.
                                               Homo sapiens
                                                                                                                                                             EP-874047-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Claim 3; Pages 17-18; 20pp; English.

The present sequence encodes a human 7-transmembrane receptor protein designated HWTMF81. HWTMF81 polypeptides and polynucleotides can be used in the treatment of infections such as bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2. They can also be used to treat pain, cancers, anorens, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, hypertrophy and psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias such as Huntington's disease or Gilles della Tourett's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The tumour rejection antigen precursor (TRAP) is processed to a tumour rejection antigen precursor (TRAP) is processed to a tumour rejection antigen (TRA) presented by HLA-A2 molecules. TRA is used to generate cytotoxic T lymphocytes for treating cancer (esp. melanoma). It can also be used to raise specific antibodies, and when complexed with HLA-A2, it can be used to prduce vaccines. Cytotoxic T lymphocytes so generated can be used in adoptive transfer or generated, or they can be generated in vivo by using vector containing the appropriate gene or using TRA or TRAP together with an adjuvant that facilitates entry into HLA-A2 presenting cells. Diagnostic methods involving the detection of expression of TRAP Sequence 13585 BP; 2857 C; 2968 G; 3894 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is 4.7-5.3 kilobases in length
this region has not been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour rejection antigen precursor coding sequence.

Tumour rejection antigen precursor; TRAP; TRA; melanoma; cancer; tumour; treatment; detection; vaccine; HLA-A2; adoptive transfer; T cell; T lymphocyte; human leukocyte antigen: ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic DNA encoding a tumour rejection antigen precursor - processed to antigen presented by HLA-A2, useful for treating or diagnosing melanoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "Unidentified nucleotide."
9422. .9456
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/note= "Unidentified nucleotide."
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; Mismatches
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Boon-falleur T, Brichard V, Coulie
Traversari C, Van PEL A, Wolfel T;
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but the sequence of
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T11549;
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/*tag= b
/note= "This r
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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10-JAN-1995; US-370319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
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WPI; 96-097390/10.
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EST clone D1160.
Human: secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; heemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
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                                                                                                                                                                                                                                                  Score 14.2; DB
Pred. No. 96;
0; Mismatches
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; Mismatches
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84.2%; Pred. No. 51
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1210000
1310000
1410000
1510000
1610000
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910000
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84.2%;
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600001
700001
800001
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1000001
1100001
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1300001
1400001
1500001
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10-APR-1997; US-838821.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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WO9845436-A2.
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V21209_10
V21209_11
V21209_13
V21209_13
V21209_14
V21209_15
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17 fragments LOCUS V21209 Accession V21209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New esterase from Aspergillus niger - useful for, e.g. feed and food processing, treating fabrics or for producing antioxidant, a processing, treating fabrics or for producing antioxidant, a processing, treating fabrics or for producing antioxidant.

T photoprotective or antioxidammatry agents
Claim 6: Fig 5A-C: 40pp: English.

This DNA sequence corresponds to the gene encoding a novel 39 kDa ferulic acid esterase (FAE, see W56728) of Aspergillus niger. It was isolated from A. niger genomic DNA using a partial gene fragment (see V28496) as probe. The invention provides vectors that include the DNA sequence, host cells transformed with the DNA or vectors, fermentation broths comprising such host cells, and esterase proteins expressed by the host cells. The FAE can cleave the ester linkage of phenolic esters. It can be used in a claimed cet esteries. FAE gene fragments can be used as probes to isolate homologous sequences having esterase activity.

Sequence 2436 BP; 633 A; 615 C; 574 G; 614 T;
                                                         Gaps
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                 DB 1; Length 13585;
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                                                                                                                                                                                                                                                            28-AUG-1998 (first entry)
Aspergillus niger ferulic acid esterase gene.
Ferulic acid esterase, esterolytic enzyme; feed supplement;
fabric; yarn; textile; ss.
Aspergillus niger.
                                                     3; Indels
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                                                                                                                                                                                                                                                                                                                                                                            519. .1421
/*tag= a
/note= "includes an intron"
519. .581
           71.0%; Score 14.2; E
84.2%; Pred. No. 78;
tive 0; Mismatches
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Best Local Similarity 84.2%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches
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Begin
                                                                                                            Db 10375 TACCTTCCGTGTATTGATT 10393
                                                                                                                                                                                                                        V28496 standard; DNA; 2436 BP
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                                                                                          2 TACCTICGAGIATACATI 20
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/*tag= c
                               Local Similarie,
hes 16; Conservative
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29-SEP-1997; U17614.
30-SEP-1996; US-722713.
(GEMV ) GENENCOR INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Norneman WS, Bower BS;
WPI; 98-240093/21.
P-PSDB; W56728.
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V21209_07
Continuation (8 of 17) of WP Sequence split into 17
WP Fragment Name
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V21209_01
V21209_02
V21209_03
V21209_04
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               Query Match
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                                                   Matches
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V28496
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Claim 1; Page 569-573; 3271pp; English.

Claim 1; Page 569-573; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences

C f the Invention. The DNA sequences are recorded on a computer readable

C medium, preferably selected from a floppy or hard disk, random access

memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using

CC the Staureus DNA sequences allows putative functions to be assigned so

that protein-encoding or regulatory regions of commercial, therapeutic or

industrial importance can be obtained. Specifically, sequences which are

consistent to encode antigens have been identified and these polypeptides can

be used in a vaccine composition against S. aureus infection. The

colypeptides can also be used in a kit for the immunodetection of

colypeptides can also be used in a kit for the immunodetection of

colypeptides can also be used in a kit for the immunodetection of

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colypeptides can also be used in a kit for the immunodetection of

colypeptides can also be used in a kit for the immunodetection of

colypeptides of any of the polypeptides. The new DNA sequences

condition to organisms transformed with the DNA sequences

condition to organism the S. aureus DNA sequences contained on the
                                                                                                                                                                                                                                                       the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence."
                                                                                                                                                                                                                                                                                                                                                                 "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                         given in the specification for this DNA sequence
16-MAR-1999 (first entry)
Staphylococcus aureus contig SEQ ID #92.
Computer readable medium; vaccine; S.aureus infection; immunodetection;
cellulitis; eyelld infection; food poisoning; osteomyelitis; therapy;
skin infection; surgical wound infection; scalded skin syndrome;
toxic shock syndrome; ds.
                                                                                                                                                                                  421 .480
/*tag- a
/note- "these bases represent a line of missing text in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1960 T;
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Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 805 G;
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                                                                                                                                                               Location/Qualifiers
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/note= "t
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30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
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                                                                                                                                       Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_f@ature
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                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
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Claim 1, Page 1412-1415; 2084pp; English.

A computer readable medium has been developed which his recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for inagnosing Enterococcus faecalis in samples. They can also be used for inagnosing Enterococcus faecalis, or commercial intection in an animal and monitoring collises on of disease, and for identifying agents which can be used to another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal

12.NOV-1998.
14.MAY-1998; U08985.
14.MAY-1997; US-046609.
16.MAY-1997; US-046655.
(HUMA-) HUMAN GENOME SCI INC.
BARABA SC, Dillon PJ, Kunsch CA;
WPI; 99-045171/04.
New isolated Enterococcus faccalis polynucleotides and polypeptides.

Enterococcus faecalis genome contig SEQ ID NO:322. Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.

Enterococcus faecalis. WO9850555-A2.

X13259/c ID X13259 standard; DNA; 5069 BP.

(first entry)

19-MAR-1999

used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus

infection.

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Gaps

.. 0

71.0%; Score 14.2; DB 1; Length 5069; 84.2%; Pred. No. 70; ive 0; Mismatches 3; Indels 0

Query Match 71.0 Best Local Similarity 84.2 Matches 16; Conservative

1384 T;

1171 G;

892 C;

1620 A;

5069 BP;

infection.

Sequence

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- useful
                                                                                                   27-APR-1998 (first entry)
Mouse metastasis-associated antigen p150 cDNA.
Antigen; p150; metastasis; tumour; cancer; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                   Mouse and human metastasis-associated p150-derived antigens for raising antibodies for therapy and diagnosis of tumours
                                                                                                                                                                Location/Qualifiers
128. .4159
                                                                  V12500/c
ID V12500 standard; cDNA; 5137 BP.
            1118 TCCCTCCCGAGTATACAAT 1100
2 TACCTICCGAGTATACATT 20
                                                                                                                                                                                                                                   GB-004161.
US-016487.
                                                                                                                                                                                                         06-NOV-1997.
18-APR-1997; E01963.
28-FEB-1997; GB-0041
                                                                                                                                                                                                                                                          (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                           WPI; 97-549725/50.
P-PSDB; W31866.
                                                                                                                                                                                                 WO9741221-A1.
                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                              29-APR-1996;
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                                                         RESULT 10
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Gaps

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DB 1; Length 6022; 3; Indels

Score 14.2; DE Pred. No. 71; 0; Mismatches

71.08;

Query Match
Best Local Similarity 84.2\*
Matches 16; Conservative

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5507 TACTITCCTIGIATACATI 5525

2 TACCTICCGAGIATACATT 20

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Claim 4; Page 41-51; 111pp; English.

This cDNA clone codes for novel murine 150 kDa cell surface metastasis-associated antigen (see Wil866), designated p150. The protein was identified by raising antisera to membrane associated proteins and assessing cross-reactivity with transformed sociated proteins and assessing cross-reactivity with transformed associated proteins and assessing cross-reactivity with transformed cost cells. An oligonuclectide based on an isolated peptide of p150 was then used to screen a mouse melanoma B16F1 library, yielding a partial p150 cDNA clone. The missing 5' sequence was chained by RACE. The CDNA sequence (see T93627) of the human homologue of p150 (see Wil867) was also obtained. A claimed method for determining the metastatic potential of a tumour cell comprises of assessing the level of p150 expression in the cell, a higher level of p150 expression in the cell, a higher level of p150 expression and consequently a higher metastatic potential. Claimed p150 nucleic acids can be used in the recombinant production of p150 polypeptides, as well as in methods for the diagnosis and sequence 5137 BP; 1164 A; 924 C; 1355 G; 1194 T;
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The present sequence, a transforming growth factor beta (TGF-beta) binding ligand, was identified by Systematic Evolution of Ligands by Exponential enrichment (SELEX). Briefly a candidate mixture of nucleic acids was contacted with TGF-beta, and nucleic acids having an increased affinity to TGF-beta partitioned from the maplified to yield a mixture of nucleic acids enriched for amplified to yield a mixture of nucleic acids enriched for sequences with higher affinity and specificity for binding to sequences with higher affinity and specificity for binding to sequences with higher affinity and specificity for binding to epithelial cell proliferation, or in the diagnosis and treatment of TGF-beta mediated pathological conditions, e.g. fibrotic conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "all pyrimidines are 2'-fluoro modified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transforming growth factor beta binding ligand lib3 13.
Transforming, growth factor, beta; TGF-beta; binding ligand;
Transforming, growth factor, beta; TGF-beta; binding ligand;
identification; SELEX; anti-mitogenic; inhibition, cell;
Systematic Evolution of Ligands by Exponential enrichment;
epithelial; prolliferation; diagnosis; treatment; fibroids;
kidney, lung; liver; dermal scarring; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.0%; Score 14; DB 1; Length 5137; 100.0%; Pred. No. 90; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T65154 standard; RNA; 125 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-1996.
30-MAY-1996; U08014.
02-JUN-1995; US-458423.
05-JUN-1995; US-465594.
05-JUN-1995; US-465591.
07-JUN-1995; US-479783.
07-JUN-1995; US-479725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701 CCTTCCGAGTATAC 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CCTTCCGAGTATAC 17
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T65154
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                                                                                                                      Gaps
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/note= "all pyrimidines are 2'-fluoro modified"
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        and more acute
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Transforming growth factor beta binding ligand lib3 3.

Transforming, growth factor; beta; binding ligand; identification; SELEX; anti-mitogenic; inhibition; cell; systematic Evolution of Ligands by Exponential enrichment; epithelial; prollferation; diagnosis; treatment; fibroids; tidney; lung; liver; dermal scarring; restenosis; ss.
                                                                                     DB 1; Length 125;
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                                                                                                                     Indels
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such as fibroids of the kidney, lung and liver and conditions such as dermal scarring and restenosis. Sequence 125 BP; 25 A; 27 C; 46 G; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                     4; Mismatches
                                                                                     Score 13.8; 1
Pred. No. 77;
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Claim 15; Page 108; 209pp; English.
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                                                                                     69.08;
                                                                                                  64.78;
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05-JUN-1995; US-465591.
07-JUN-1995; US-479783.
07-JUN-1995; US-479783.
20-MAR-1996; US-418693.
(NESS-) NESTAR PHARM INC.
                                                                                                                                                 2 TACCTTCCGAGTATACA 18
                                                                                                                                                                  36 UAGCUUCCGAGUAGACA 52
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                                                                                                                     Conservative
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Best Local Similarity 64.7
Matches 11; Conservative
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US-458423.
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Best Local Similarity
Matches 11; Conserv
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02-JUN-1995;
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RESULT

us-09-037-472-2.rng

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The present sequence, a transforming growth factor beta (TGF-beta)

The present sequence, a transforming growth factor beta (TGF-beta)

binding ligand, was identified by Systematic Evolution of Ligands

by Exponential enrichment (SELEX). Briefly a candidate mixture of

nucleic acids was contacted with TGF-beta, and nucleic acids

having an increased affinity to TGF-beta partitioned from the

cemainder of the mixture. The partitioned nucleic acids were then

amplified to yield a mixture of nucleic acids enriched for

captences with higher affinity and specificity for binding to

TGF-beta. The ligand is anti-mitogenic and may be used to inhibit

cepithelial cell proliferation, or in the diagnosis and treatment of

TGF-beta mediated pathological conditions, e.g. fibrotic conditions

such as fibroids of the kidney, lung and ilver and more acute

conditions such as dermal scarring and restenosis.

Sequence 116 BP; 24 A; 27 C; 44 G; 21 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence, a transforming growth factor beta (TGF-beta)
binding ligand, was identified by Systematic Evolution of Ligands
                                                                                                                                                                                                                                                                        Identification of nucleic acid ligands to TGF-beta, PDGF and hKGF
                                                                                                                                                                                                                                                                                         using SELEX, used in the diagnosis and treatment of proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pagratis N, Ringquist S, Toothman PJ;
                                                                                                                                                                                                                            Gold L, Janjic N, Pagratis N, Ringquist S, Toothman PJ;
WPI; 97-034387/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ification of nucleic acid ligands to TGF-beta, SELEX, used in the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 109; 209pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.0%;
64.7%;
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Gold L, Janjic N, Pagrat
WPI; 97-034387/03.
                                                                                                                                                                                                          (NEXS-) NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TACCTTCCGAGTATACA 18
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Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                05-JUN-1995; US-465594.
05-JUN-1995; US-465591.
07-JUN-1995; US-479783.
07-JUN-1995; US-479725.
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                                                                               02-JUN-1995;
05-JUN-1995;
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Claim 15; Pages 108-109; 209pp; English.

The present sequence, a transforming growth factor beta (TGF-beta)

Chinding ligand, was identified by Systematic Evolution of Ligands

by Exponential enrichment (EEEEX). Briefly a candidate mixture of

nucleic acids was contacted with TGF-beta, and nucleic acids

having an increased affinity to TGF-beta partitioned from the

remainder of the mixture. The partitioned nucleic acids were then

amplified to yield a mixture of nucleic acids enriched for

sequences with higher affinity and specificity for binding to

TGF-beta. The ligand is anti-mitogenic and may be used to inhibit

cepithelial cell proliferation, or in the diagnosis and treatment of

TGF-beta mediated pathological conditions, e.g. fibrotic conditions

such as fibroids of the kidney, lung and restenosis.

Conditions such as dermal scarring and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                              /*tag= a
/note= "all pyrimidines are 2'-fluoro modified"
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/note= "all pyrimidines are 2'-amino modified"
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Transforming growth factor beta binding ligand lib4 32.
Transforming, growth factor; beta, TGF-beta, binding ligand; identification; SELEX: anti-mitogenic; inhibition; cell; Systematic Evolution of Ligands by Exponential enrichment; epithelial; proliferation; diagnosis; treatment; fibroids; Kidney; lung; liver; dermal scarring; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 125;
                                                               10-SEP-1997 (first entry)
Transforming growth factor beta binding ligand lib3 4.
Transforming, growth factor; beta; TGF-beta; binding ligand; identification; SELEX: anti-mitogenic; inhibition; cell; Systematic Evolution of Ligands by Exponential enrichment; epithelial; proliferation; diagnosis; treatment; fibroids; kidney; lung; liver; dermal scarring; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEXS.) NEXSTRE PHARM INC.
GOLd L. Janjic N. Pagratis N. Ringquist S. Toothman PJ;
WPI: 97-034387/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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1. .125
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64.7%;
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                        T65156 standard; RNA; 125
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05-JUN-1995; US-465594.
05-JUN-1995; US-465591.
07-JUN-1995; US-479783.
07-JUN-1996; US-479725.
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US-458423.
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                      WO9638579-A1
                                                             10-SEP-1997
                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders
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Gaps

ö

Indels

Length 116;

DB 1;

PDGF and hKGF proliferative

T65157;

RESULT 14 T65157

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CC by Exponential enrichment (SELEX). Briefly a candidate mixture of concleic acids was contacted with TGF-beta, and nucleic acids having an increased affinity to TGF-beta partitioned from the remainder of the mixture. The partitioned nucleic acids were then concerned to yield a mixture of nucleic acids enriched for amplified to yield a mixture of nucleic acids enriched for consequences with higher affinity and specificity for binding to consistent and is anti-mitogenic and may be used to inhibit consistent and is anti-mitogenic and may be used to inhibit consistent and proliferation, or in the diagnosis and treatment of TGF-beta mediated pathological conditions, e.g. fibrotic conditions contains of the Xidney, lung and liver and more acute conditions such as fibroids of the Xidney, lung and restenosis.

CC Such as fibroids of the Xidney, lung and restenosis.

CC conditions such as dermal scarring and restenosis.

CC conditions such as dermal scarring and restenosis.

CC sequence 123 BP; 24 A; 28 C; 45 G; 1 T; 25 U;

Autches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QV 2 TACCTTCCGAGTATACA 18
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Search completed: September 18, 1999, 05:27:15 Job time: 1680 sec

:| |::||||:| |||| 34 UAGCUUCCGAGUAGACA 50

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM nucleic · nucleic search, using sw model

8 ; Search time 1405 Seconds (without alignments)
28.079 Million cell updates/sec September 18, 1999, 06:47:28 Run on:

2546578 seqs, 986266752 residues US-09-037-472-2 20 1 GTACCTTCCGAGTATACATT 20 IDENTITY\_NUC Title: Perfect score: Scoring table: Sequence: Searched:

em\_est1:\*
em\_est2:\*
em\_est3:\*
em\_est4:\*
em\_est5:\*
em\_est7:\*
em\_est7:\*
em\_est9:\*
em\_est9:\* em\_estll: em\_estl2: em\_estl3: em\_estl5: em\_estl6: em\_estl8: em\_estl8: em\_estl8: em\_estl8: em\_estl9: em\_estl9: ESI:\* Database :

9D-est4:\*\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	õ	83140 mt78h0	616584 zehn02	A144931 mr70e0	492993 vi70al	193066 vi67h0	A766803 0a37g1	I071047 UI-R-C	1075980 ov47a0	414455 mb18a0	026016 AV0260	728374 RNTCH1	731481 BNLGH	618964 AEMTBL	638935 AEMTA	T68771 yc29b01.r	265/ HUMU89E	3483 y418603	982748 uh15b	239229 GM121	535840 jun2.	556178 UI-R-	3/2253 te39D 3971 1037 1ª	5099 va95r03	145382 mr7891	715	A909452 ol14dl	390320 mx03d1	1449905 mr/8g1 1660458 we67d0	33798 CELKO36C	04514 pk24f06.	66346 yc78b12.	27 Yc93g09.	11528 ym10a02.	49582 Ygb8g11. 50886 wq70d01	51427 vg72e07.	51659 va73b04.	62734 HUM320C0	
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## ALIGNMENTS

AA183140 447 bp mRNA EST 07-JAN-1997 mt78h05.rl Soares mouse lymph node NbMLN Mus musculus cDNA clone IMAGE:636057 5', mRNA sequence.
AA183140 g1766796
AA183140.1 G1:1766796 RESULT 1 AA183140/C LOCUS DEFINITION ACCESSION NID VERSION

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1...187
/organism="Danio rerio"
/db_xref="textain: pario"
/db_xref="textain: pario"
/db_xref="textain: pario"
/db_xref="textain: pario"
/dev_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XLI-Blue mrF"
/note="Organ: heart; Vector: Lambda ZAP Express; Site_1:
/note="Organ: heart; Vector: Lambda ZAP Express; Site_1:
EcoRI; Site_2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Ollgo dr adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 505)
Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                         Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA144931 505 bp mRNA EST 11-FEB-1997
mr70e01.rl Stratagene mouse testis (#937308) Mus musculus cDNA
clone IMAGE:602808 5' similar to TR:G285949 G285949 ORF, COMPLETE
CDS: ;, mRNA sequence.
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinoides; Lo 187)

Ton, C., Mably, J. D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                        Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced g1:1288690.
                                                                                                                                                                                                        On Jun 5, 1998 this sequence version replaced gi:3188599
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                                                                                                                                                                                                                                                                                                                                                                                                                               PCR PRIMERS
FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGAATACGACTCACTATAAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
LOCATION/Qualifiers
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Pred. No. 71;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                               Email: liewcc@utcc.utoronto.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA144931.1 GI:1714305
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89.5%;
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                             Tel: 4169788758
Fax: 4169785650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zebrafish.
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
                          Mus musculuse.

Mus musculuse.

Mus musculuse.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases I to 447)

Marray, Hillier, L. Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and

Materston, R.

The WashU-HHMI Mouse EST Project
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0
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Zehn0293.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio
CDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                          Unpublished (1996)
On Nov 29, 1993 this sequence version replaced gi:430246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 447;
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/sex="male"
/tissue_type="lymph node"
/dev_lage="4 weeks"
/lab_nost="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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90.0%; Pred. No. 21;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGG1388049
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 427.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:636057"
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA492993 445 bp mRNA EST 25-JUN-1997 vi70a10.rl Stratagene mouse testis (#937308) Mus musculus CDNA clone IMAGE:917562 5' similar to TR:G285949 G285949 ORF, COMPLETE
                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .: mouseest@watson.wustl.edu clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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On Sep 12, 1996 this sequence version replaced gi:1407297
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="Inbred CD-1"
/db_xrt taxon:10090"
/clone="IMAGE:602808"
/clone_lib="Stratagene mouse testis (#937308)"
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This clone is available royalty-free through LLNL: conf
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Pred. No. 1.5e+02;
); Mismatches 3; Indels 0
                                                                                                                                                                     Possible reversed clone: similarity on wrong strand Seq primer: -20ml3 rev1 ET from Amersham High quality sequence stop: 336. Location/Qualifiers
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Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
The WashU-HHMI Mouse EST Project
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AA492993.1 GI:2222555
                                                                                                                                                                                                                                                                                                                                                               /sex="males"
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AA492993
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85.0%;
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Best Local Similarity 85.0
Matches 17; Conservative
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                                                                                                                                                    MGI:368240
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ORIGIN
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DEFINITION
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AA492993/c
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COMMENT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                       AA493066 392 bp mRNA EST 25-JUN-1997 v167h04.rl Stratagene mouse testis (#937308) Mus musculus CDNA clone IMAGE:917335 5' similar to TR:G285949 G285949 ORF, COMPLETE
Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further infommation.
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                    mouse testis (#937308)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 445;
           MOI:529778

Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 revl ET from Amersham High quality sequence stop: 175.

Location/Qualiflers
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85.0%; Pred. No. 1.5e+02;
Live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: .28ml3 revl ET from Amersham
                                                                                                                                  1. 445
'Organism="Mus musculus"
'Strain="Inbred CD-1"
'db_xref="taxon:10090"
'Clone="!rAGE:917562"
'Clone="!rAGE:917562"
'Sex="males"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism~"Mus musculus"
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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AA493066.1 GI:2222628
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AA493066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GTACCTTCCGAGTATACATT
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Program for Rat Gene Discovery and Mapping
University of lowa
451 Eckstein Medical Research Building lowa City, IA 52242, USA
741: 319 335 8250
Fax: 319 335 9565
Fax: 310 335
/strain="sprague-Dawley"
/db_xef="taxon:10116"
/clone=lib="UI-R-C1"
/clone_lib="UI-R-C1"
/dev_stage="Adult"
/lab host="BHI0B (life Technologies)"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
/note="vector is IT is lee_1: Not I; site=2: Eco RI; The UI-R-C1
library is a subtracted library derived from the UI-R-C1
library, which is a subtracted library derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 292)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI071047 292 bp mRNA EST 11-FEB-1999
UI-R-CL-lo-a-10-0-UI.S1 UI-R-CI Rattus norvegicus CDNA clone
UI-R-C1-lo-a-10-0-UI 3', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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85.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 3;

    .292
    /organism="Rattus norvegicus"

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AI071047.1 GI:3396152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 85.09
Matches 17; Conservative
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AUTHORS
TITLE
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COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                AA766803 428 bp mRNA EST 08-FEB-1998 oa37g12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1307206 3/ similar to gb:X74301_cds1 MHC CLASS II TRANSACTIVATOR CLITA (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 428)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1918)
On Jan 19, 198 this sequence version replaced gi:2150542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                       /clone="IMAGE:917335"
/clone=1ib="Stratagene mouse testis (#937308)"
/sex="males"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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/clone=11b="MOI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.2; DB 34;
Pred. No. 1.5e+02;
0; Mismatches 3;
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/db_xref="taxon:9606"
/map="7; 21q"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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AA766803.1 GI:2818041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%;
85.0%;
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Matches 17; Conserv
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ORIGIN
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/Clone_lib="Scares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/dev_stage="19.5 dpc total fetus"
/dev_stage="19.5 dpc total fetus"
/dev_stage="19.5 dpc total fetus"
/note="Vector: p77130 (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI: 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                          Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Mammalia; Butheria; Rodenita; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 367)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This clone was previously sequenced on the 5' end only, this new data is from the 3' end data is from the 3' end end data is from the 3' end Location (location) and ity sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Apr 21, 1998 this sequence version replaced gi:3072429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI414455 367 bp mRNA EST 09-FEB-1
mb18a02.x1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:329738 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%; Score 15.2; DB 42; Length 452; 85.0%; Pred. No. 1.5e+02; Live 0; Mismatches 3; Indels 0.
                 /clone_lib="Soares_testis_NHT"
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/db_xref="taxon:10090"
/map="4p16.3; 3; X"
/clone="IMAGE:329738"
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UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, and ut lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-E1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dI track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C1) was constructed as follows: PCR amplified cDNA inserts from UI-R-C0 clones from which 8. ESTs had been derived was used as a driver in a hybridization with the UI-R-C0 library in the form of single-stranded circles. The remaining single-stranded circles. The remaining single-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C1 library. This procedure has been previously described, when a contract of contracts the UI-R-C1 library. This procedure has been previously described.
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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4047a06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640434

37, mRNA sequence.

A1075980
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia;
Butheria: Primates: Catarrhini: Hominidae: Homo.
1 (Dases 1 to 452)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
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Unpublished (1997)
On Jan 17, 1998 this sequence version replaced g1:2045249.
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/db_xref="taxon:9606"
/clone="IMAGE:1640434"
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AI075980.1 GI:3405158
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Best Local Similarity 85.0
Matches 17; Conservative
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AV026713/c
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 149)
Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Ito,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,
Hara,A., Hayatsu,M., Hori,F., Ishikawa,T., Itoh,M., Izawa,M.,
Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y.,
Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y.,
Tominaga,N., Matanabe,S., Yaqame,M., Yamamura,T., Yokota,T.,
Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
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Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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               double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Br. Minoru Ko (Mayne State University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV026016 149 bp mRNA EST 02-JUN-1999
AV026016 Mus musculus adult C57BL/6J lung Mus musculus cDNA clone
rgitaccaaicigaagigggagcggccgcaffifitiffffffffffff 3'],
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On Mar 8, 1999 this sequence version replaced gi:4388523
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/clone="1200017F23"
/clone_lib="Mus musculus adult C57BL/6J lung"
/tissue_type="lung"
                                                                                                                                                                                                                                                                                    Query Match 76.0%; Score 15.2; DB 46; Length 367; Best Local Similarity 85.0%; Pred. No. 1.5e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0;
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
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/db_xref="taxon:10090"
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36 c 30 g
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AV026016/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mus. Eukaryota; Metazoa; Sciurognathi; Muridae; Murinae; Mus. Eutheria; Rodentia; Sciurognathi; Muridae; Mus. at 1 (Dases 1 to 257)

Carninci, P., Shibata, K., Ozawa Y., Konno, H., Ito, M., Aizawa. K., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishigawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Saloc, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Sizuki, H., Tateno, M., Tomaru, Y., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. RIKEN Mouse ESTS

N. Unpublished (1999)

On May 18, 1998 this sequence version replaced gi:3138575.
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S. A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
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W1026713 Mus musculus adult C57BL/6J liver Mus musculus cDNA clone
1300020808, mRNA sequence.
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/clone="1300002B08"
/clone=11b="Mus musculus adult C57BL/6J liver"
/tissue_type="liver"
/dev_stage="adult"
56 c 64 q 64 t
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Length 149;
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85.0%; Pred. No. 1.5e+02;
live 0; Mismatches 3;
   76.0%; Score 15.2; DB 50;
85.0%; Pred. No. 1.5e+02;
                                                                  0; Mismatches
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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1. .257
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                                                                                                                               1 GTACCTTCCGAGTATACATT 20
                                                                                                                                                              100 GAACTITCCGAGIATACAAT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 81-298-36-9145
Fax: 81-298-36-9098
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Best Local Similarity 85.08
Matches 17; Conservative
         Query Match 76.0°
Best Local Similarity 85.0°
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
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Aedes aegypti
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota; Meoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Culicidae; Aedes.
1 (bases 1 to 614)
6ill,S.S., Ross,L.S. and Wadiak,H.
Gill,S.S., Ross,L.S. and Wadiak,H.
Expressed sequence tags of cDNA clones from an enriched Malpighian tubule and gut library from Aedes aegypti
Unpublished (1999)
On Mar 10, 1998 this sequence version replaced gi:2948045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEMTBL29 Aedes aegypti MT pSPORT Library Aedes aegypti cDNA clone AI618964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; The
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/organism="Aedes aegypti"

/db_xref="taxon:7159"

/clone="BL29"

/clone_lib="Aedes aegypti MT pSPORT Library"

/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="malpighian tubules and gut"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                       /ultivar="Acala Maxxa"
/db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="X11-Blue"
/note="Vector: pBluescript II KS+"
8 a 109 c 138 g 170 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.0%; Score 15.2; DB 51;
85.0%; Pred. No. 1.5e+02;
Live 0; Mismatches 3;
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Environmental Toxicology
University of California, Riverside
1479 Boyec Hall, Riverside, CA 92521, USA
Tel: 909 787 3547
Fax: 909 787 3087
                                                                                                                                                                                                      1. 625
/organism="Gossypium hirsutum"
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Seg primer: CCAAGCTCTAATACGACTCACTAT
High quality sequence stop: 600.
Location/Qualifiers
             Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burre@nlux.bnl.gov
                                                                                                                                                             Seq primer: T3 Primer.
Location/Qualifiers
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Best Local Similarity 85.0
Matches 17; Conservative
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AI618964
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AI728374/C
LOCUS AI728374 611 bp mRNA EST 11-JUN-1999
DEFINITION BULGH110609 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to (AJ000478) cytochrome P450 [Helianthus tuberosus], mRNA
                                                                                                                                                                                                                                Gossypium hirsutum
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 611)
Elewitt.M., Matz.E.C., Davy,D.F. and Burr,B.
ESTS from developing cotton fiber
Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3188157.
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Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Majooliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 625)
Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
ESTS from developing cotton fiber
Unpublished (1999)
On Mar 10, 1998 this sequence version replaced gi:2948292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI731481 625 bp mRNA EST 11-JUN-1999
BNLGH19879 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to (AJ000478) cytochrome P450 [Hellanthus tuberosus], mRNA
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Corganism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
/cultivar="Acala Maxxa"
/db.xref="taxon:3635"
/clone_lib="six-day Cotton fiber"
/tissue_type="limmature fiber"
/dev_stage="six days post anthesis"
/lab_host="XII-Blue"
/note="Vector: pBluescript II KS+"
2 a 105 c 136 g 168 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burrébnlux1.bnl.gov
Seq primer: T3 Primer.
                                                                                                                                               95047226
AI728374.1 GI:5047226
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Biology Department
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Best Local Similarity 85.0 Matches 17; Conservative
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AI731481
g5050333
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AI731481/C
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Contact: Gill SS
Environmental Toxicology
University of California, Riverside
5419 Boyce Hall, Riverside, CA 92521, USA
Tel: 909 787 3547
Fax: 909 787 3587
Email: sarjeet.gill@ucr.edu
Seq primer: CCAAGCTCTAATACGACTCACTAT
High quality sequence stop: 635.
Location/Qualifiers
irce
/ Coranism="Aedes aegypti"
/ Actor="Aedes aegypti"
/ Actor="Aegypti"
/ Acto
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yellow fever mosquito.

Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Meoptera; Endopterygota; Diptera; Nematocera;

Culicoidea; Culicidae; Aedes.

1 (bases 1 to 635)

Gill,S.S., Ross,L.S. and Wadiak, H.

Expressed sequence tags of cDNA clones from an enriched Malpighian tubule and gut library from Aedes aegypti

Unpublished (1999)

On Mar 16, 1998 this sequence version replaced gi:2961689.
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AEMTAL76 Aedes aegypti MT pSPORT Library Aedes aegypti cDNA clone
AL76 5', mRNA sequence.
AIG38935
cDNA was cloned into the Sall/NotI sites of pSPORT1." $^{\circ}$ 110 c $^{\circ}$ 162 g ^{\circ} 184 t
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                                                                                                                                                                                   Query Match 75.0%; Score 15; DB 49; Length 614; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 15; Conservative 0; Mismatches 0; Indels
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Job time: 3649 sec
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A1638935.1 GI:4691169
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     357 TTCCGAGIATACATT 371
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Perfect score:

Sequence:

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Scoring table:

Database : Searched:

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AC006804 Caenorhab
AC006802 Caenorhab
AC006847 Mus muscu
AL022170 Homo sapi
AC002115 Human DNA
M13212 Chicken car
L31504 Neurospora
AC003029 Homo sapi
AC03029 Homo sapi
AC03029 Homo sapi
AC0329 Homo sapi
AC030476 Carcila sapi
AC030476 Gazella caenorhab
AF030476 Gazella sapi
AF030476 Gazella sapi
AF030478 Gazella sapi
AF030480 Gazella sapi
AF030480 Gazella dapi
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297209 S.pombe chr
AF038122 Podospora
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AL034390 I
AC007778 H
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AC004823
AC006398
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown.
Unknown.
Unclassified.
Unclassified.
I (bases 1 to 22)
Kornman, K.S. and Duff,G.W.
Rotenting genetic predisposition to periodontal disease Patent: US 5686246-A 1 11-NOV-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 22;
                                                                                                                                                                                                                                                                                                                                                                                     PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
2.2;
                                                                                                                                                                                                                                                                                                                                                                           22 bp DNA
Sequence 1 from patent US 5686246.
173225
g3009364
173225.1 GI:300026
                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                            AC006812
AC006812
HSAC001232
                                     HS501N12
HSAC002115
CHKLNKPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22;
Pred. No.
                                                           CHKLNKPA2
NEURO1DHC
AC003029
HS856G1
AC004340
AC004767
ATV038
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SPAC19G12
AF038122
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AB002762
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AC004823
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171336
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                                                    September 18, 1999, 15:25:20 ; Search time 436.05 Seconds
(without alignments)
196.923 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
          GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                 US-09-037-472-1
27
1 AAGCTTGTTCTACCACCTGAACTAGGC 27
                                                                                                                               679419 seqs, 1590154680 residues
                                        using sw model
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Homo sapi Leishmani sapi

Homo

23-DEC-1997

Schore 22

Result No.

Homo sap

Human mRNA

SOURCE

RESULT

ò QQ

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Submitted (23-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA
Mo 1909, USA
Mo 1999 this sequence version replaced gi:4263134.
MoTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the places
is not known and their order in this sequence record is a arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Waterston, R.H.
The sequence of Caehorhabditis elegans clone
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Anote="polyA site"

11863. .11970

/note="Alu repetitive sequence"

2226 g 3547 t
                                                                                                                                                     repetitive sequence"
                                                                                                                                                                                                                                                                                                                            9466. 8483
/note="poly|dA-dC] tract"
8912. 9137
/note="5 x 46 bp repeat"
9770. 9806
/note="poly [dT-dG] tract"
10290. 11643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22; DB 1 Pred. No. 2.1; 0; Mismatches
                                                                                                                                                                                              6433. 7814
/number=5
7695. 7744
/note="poly [dA-dC] tract"
7815. 7939
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100.0%; Prf
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Caenorhabditis elegans
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HTG; HTGS_PHASE1.
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Waterston, R.H.
                                                                                                                               4893. .5174
/note="Alu re
6262. .6432
                                                                                                                                                                                                                                                                                              7940. .10289
                                                                                                   .6261
                                                    /number=3
                                     .4102
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Best Local Similarity 100.
Matches 22; Conservative
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarhini; Hominidae; Homo.
1 (bases 1 to 11970)
Furutani,Y., Notake,M., Fukui,T., Ohue,M., Nomura,H., Yamada,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SWISS_PROT:P01583"
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DBAWKFDMGAYKSSRDDAKTTVILRISKTQLYVTAQDEDOPVLLKBMPEIRYTITGSE
1208. 3165
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erratum:[[published erratum appears in Nucleic Acids Res 1986 Jun
25,14(12):5124]]
                                                                                                                                                                                                                                                                                                                                                                      Complete nucleotide sequence of the gene for human interleukin 1
                                                                                                                                                                                            933785
X03833.1 GI:33785
Alu repetitive sequence; interleukin 1 alpha; inverted repeat;
repetitive sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(1438. .1488,2153. .2207,3166. .3214,4103. .4325,6262. .6432,7815. .7939,10290. .11643)
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/codon_start=1
     Gaps
                                                                                                                                                24-APR-1993
   ..
0
     Indels
                                                                                                                                             HSILLAG 11970 bp DNA PRI
Human gene for interleukin 1 alpha (IL-1 alpha).
X03833
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   ..
   Mismatches
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/note="liverted repeat A'"
1383. .1390
/note="direct repeat 1"
1407. .1413
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1375. .1382
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/db_xref="taxon:6239"
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Caenorhabditis elegans
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HTG; HTGS_PHASE1.
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84.0%;
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Best Local Similarity 84.0
Matches 21; Conservative
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Best Local Similarity 84.0
Matches 21; Conservative
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Submitted (24-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
On Mar 1, 1999 this sequence version replaced gi:4263476.
* NOTE: This is a "working draft' sequence. It currently
* CONTE: This is a "working draft' sequence of the pieces
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
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Rhabditina: Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 145614)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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Caenorhabditis elegans clone Y53G8Y, WORKING DRAFT SEQUENCE,
unordered pieces.
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 145614;
                                                                                      19062: contig of 19062 bp in length 19071: gap of unknown length 27630: contig of 5559 bp in length 27639: gap of unknown length 54395: coutig of 25756 bp in length 54404: gap of unknown length 56414: contig of 2010 bp in length 56423: gap of unknown length 145614: contig of 89191 bp in length.
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                                                                                                                                                                                                                                                                                                        /organism="Caenorhabditis elegans
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/clone="Y53G8B"
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HTG; HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans
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Waterston, R.H.
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Direct Submission
Submitted (24-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 244239)
Waterston, R.H.
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Caenorhabditis elegans clone Y55D5, WORKING DRAFT SEQUENCE, 4
                                                                                                                                                                                       Length 145614;
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/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="Y53G8Y"
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84.0%; Pred. No. 79;
iive 0; Mismatches
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Homo sapiens DNA sequence from clone 501N12 on chromosome 6p21.1-23 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene. Contains ESTs, STSS
                                                                                                                                                                                                                                                                                                                                                  Wu, H., Yao, Z., McDermid, H. and Roe, B.A.
Direct Submission
Submitted (28-JAN-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eutheria; Rodentia; Sciurognathi; Muridae· Murinae; Mus.
1 (bases 1 to 151528)
Muv.H., Yao, Z., MoDermid, H. and Roe, B.A.
Mus musculus Chromosome 6 BAC Clone 67414
                                         09-JUN-1999
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ON 73019, USA
ON 199, 1999 this sequence version replaced gi:4580404.
* NOTE: This is a "working draft" sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                         AC006447 151528 bp DNA HTG 09-JUN-
Mus musculus, WORKING DRAFT SEQUENCE, 5 unordered pieces.
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12748: contig of 7193 bp in length
12823: gap of unknown length
37094: contig of 24201 bp in length
82029: contig of 44930 bp in length
82104: gap of unknown length
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cocation/Qualifiers
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/db_xref="taxon:10090"
1 33398 c 33443 g 41215 t
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84.0%; Pred. No. 79;
ive 0; Mismatches
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Best Local Similarity 84.0
Matches 21; Conservative
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Clone requests: clonerequect(sanger.ac.uk

On Jul 1, 1998 this sequence version replaced gi:2980811.

During sequence assembly data is comparated from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence is the entire insert of clone 501M12. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of human chromosome 6, mapping group and Armin Volz & Andreas Ziegler. Further information can be found at humin chromosome 6 mapping group and Armin Volz & Andreas Ziegler. Further information can be found at humin chromosome 6 mapping group and Armin Volz & Andreas Ziegler. Further information can be found at humin chromosome 6 mapping group and Armin Volz & Andreas Ziegler. Further information can be found at humin chromosome formed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.mac.ubd.biffalo.edu/ VECTOR: pCYPAC2.
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Aloedlksaerlmedaknsktllpnlyhvggaswagasgllsspioetlesmagevtr
VVDeolkallesmydaaenlcpnvmkkahirodlihastekisiprtfyknyllegsg
Idilnkisevklyvasflsdrivdeildalshchhkladhfsrrgktlpogesleiel
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//note="AluJb repeat: matches 280. .1 of consensus"
complement(1341. .1477)
//note="Min repeat: matches 237. .85 of consensus"
2942. .3479
//note="Li repeat: matches 1432. .1968 of consensus"
//note="Alu'i repeat: matches 1. .296 of consensus"
//note="Alu'i repeat: matches 1. .296 of consensus"
//note="Alu'i repeat: matches 1. .296 of consensus"
//note="AluJo repeat: matches 301. .1 of consensus"
//gene="AluJo repeat: matches 301. .1 of consensus"
//gene="AluJo repeat: matches 301. .1 of consensus"
//gene="AluJo repeat: matches 301. .1 of consensus"
                                                                   Tubby, B.
Direct Submission
Submitted (06-JUL-1998) E-mail enquires: humquery@sanger.ac.uk
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8239. .8475
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/note="AluSg repeat: matches 1. .239 of consensus"
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/codon_start=2
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Primates; Catarrhini; Hominidae; Homo.
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/product*dJ501N12.1"
/protein_id="cAA18156.1"
/db_xref="PID:e1312796"
/db_xref="PID:e3355565"
/db_xref="GI:3355565"
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/chromosome="6"
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1. .170952
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/clone_lib="RPCI3"
444. .516
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/gene="dJ501N12.1"
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Complement(1909). 1/42()

n 7480. 17647

n 17480. 17647

n 1840. 17647

n 18420. 19840

n 198420. 19860

n 1986
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7,000="MIR repeat: matches 35. .134 of consensus"
7,000="MIR repeat: matches 260. .77 of consensus"
28097. .28238
7,000="MIR repeat: matches 71. .201 of consensus"
28097. .28238
7,000="MIR repeat: matches 71. .201 of consensus"
7,000="match: 6SS AQ020591"
7,000="match: 6SS AQ020591"
7,000="match: 6SS AQ020591"
7,000="match: 30959]
7,000="MIRSA repeat: matches 311. .57 of consensus"
7,000="MIRSA repeat: matches 301. .1 of consensus"
7,000="MIR repeat: matches 253. .2 of consensus"
7,000="MIR repeat: matches 253. .2 of consensus"
7,000="MIR repeat: matches 299. .1 of consensus"
7,000="MIRS repeat: matches 299. .1 of consensus"
7,000="MIRS repeat: matches 146. .87 of consensus"
7,000="MIRS repeat: matches 98. .124 of consensus"
7,000="MIRS repeat: matches 1. .298 of consensus"
7,000="MIRS repeat: matches 1. .298 of consensus"
7,000="MIRS repeat: matches 30. .134 of consensus"
7,000="MIRS repeat: matches 30. .134 of consensus"
7,000="MIRS repeat: matches 30. .134 of consensus"
7,000="MIRS repeat: matches 180. .21 of consensus"
7,000="MIR repeat: matches 180. .21 of consensus"
                                                                                                                                                                                                                                                                                     //orde="match: GSS AQ016761"
complement(16512. 16606)
/note="MER21B repeat: matches 790. .703 of consensus"
complement(16545. 16637)
/note="MER39 repeat: matches 676. .582 of consensus"
complement(16603. .17427)
                                                                                                                                                        /note="Alusx repeat: matches 273. .1 of consensus" complement(10099. 10222)
/note="Alusp repeat: matches 303. .179 of consensus"
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/note="Alux repeat: matches 301. .2 of consensus"
complement(48410. .49073)
/gene="d3501N12.2"
/note="match: cDNA Y10205"
complement(8536. .8952)
/gene="dJ501N12.1"
/note="match: GSS B37778"
complement(9800. .10072)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 10374)

Lamerdin,J.E., McCready,P.M., Adamson,A.W., Burkhart-Schultz,K., Garcia,E., Kyle,A., Ramirez,M., Stilwagen,S., Garnes,J., Bonganan,L., E., Bruee,R., Quan,G., Montgomery,M., Ow,D., Kobayashi,A., Sequence analysis of a 1 Mb region in human 19q13:1

Unpublished (1997)

2 (bases 1 to 103574)
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                                                              Note="MER42c repeat: matches 348. .1536 of consensus" 50015. .50348

Note="MIR42c repeat: matches 348. .1536 of consensus" 50724

Note="MiluJo repeat: matches 2. .302 of consensus" complement(50998. .51085)

Note="MIRZ repeat: matches 145. .58 of consensus" complement(52991. .53050)

Note="MIRZ repeat: matches 699. .554 of consensus" complement(52991. .53050)

Note="MIRZ repeat: matches 234. .175 of consensus" complement(60934. .60997)

Note="MIRS repeat: matches 234. .175 of consensus" complement(60036. .61200)

Note="MIRS repeat: matches 409. .251 of consensus" complement(60039. .63317)

Note="MIRS repeat: matches 30. .142 of consensus" complement(60039. .63317)

Note="MIRS repeat: matches 48. .409 of consensus" complement(6509. .63317)

Note="MIRS repeat: matches 48. .409 of consensus" complement(6545. .65881)

Note="MIRS repeat: matches 4. .1372 of consensus" complement(6545. .66881)

Note="MIRS repeat: matches 345. .9 of consensus" complement(65491. .66232)

Note="MIRS repeat: matches 345. .9 of consensus" complement(65491. .67789)

Note="MIRS repeat: matches 345. .9 of consensus" complement(65491. .67789)

Note="MIRS repeat: matches 345. .9 of consensus" complement(65491. .67789)

Note="MIRS repeat: matches 345. .9 of consensus" complement(68957. .66232)

Note="MIRS repeat: matches 345. .9 of consensus" complement(68957. .66545)

Note="MIRS repeat: matches 345. .9 of consensus" complement(68957. .66545)

Note="MIRS repeat: matches 345. .9 of consensus" complement(6991. .67789)
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/evidence=not_experimental
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Human DNA from overlapping chromosome 19 cosmids R31396, F25451,
and R31076 containing COX6B and UPKA, genomic sequence, complete
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/evidence=not_experimental complement(48410. .49073) /gene="dJ501N12.2"
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/gene="dJ501N12.3"
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                                                                                                                                                                                                                       the right."

// map-"fibroblast."

// cell_type="fibroblast."

// map-"orientation is centromere to telomere."

// note="cosmid libraries constructed at LLNL from flow-sorted chromosomes from hybrids UV5HL9-5B and 5HL2-B, which carry chromosome 19 as their only human chromosome."

// complement(187. 466)

// rpt_family="L1"

// rpt_family="L1"

// rpt_family="L1"

// rpt_family="L1"

// rpt_family="L1"

// rpt="predicted exon, program: grail2exons_human_1.3, frame: 2 quality: good, score: 57.000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="BLASTX similarity to (283. .429); match: 0.47, score: 5.7e-29; database searched: nr; hypothetical L1 protein (third intron of gene TS)- human >prf||1510254A L1 repetitive element ORF (Homo sapiens)" /rpt_family="L1" complement(4223. .4455)
                                                                                                                                                                                            /map="19q13.1 between D19S208 and CAPNS" /map="Overlaps CH19F14121 to the left and CH19R28052 to
Direct Submission
Submitted (13-MAY-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
R31396 from 1-36,162; F25451 from 25,661-55,793; R31076 from
66,237-103,574.
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/db_xref="taxon:9606"
/clone="R31396-F25451-R31076"
/chromosome="19"
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11801. .12092
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complement(12570. .12861)
/rpt_family="ALU"
12958. .13233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1907. .2112
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/rpt_family="L9". .2280)
/rpt_family="ALU"
complement(2310. .2392)
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complement(5730. .6009)
/rpt_famlly="ALU"
complement(7534. .7834)
/rpt_famlly="ALU"
/rpt_famlly="ALU"
/rpt_famlly="ALU"
9070. .9183
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3377. . 2663
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complement(4517, 4584)
/rpt_family="ALU"
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127. .5417
                                                                                      Location/Qualifiers
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289. .1590
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rpt_family="ALU"
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rpt_family="ALU"
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429. .3705
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<3755. .4205
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 TITLE
JOURNAL
                                                                                      FEATURES
                                                    COMMENT
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/rpt_family="ALU"
complement(13377. .13672)
/rpt_family="ALU"
13899. .14179
/rpt_family="ALU"
14234. .14310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="predicted exon, program: grail2exons_human_1.3, rame: 1, quality: marginal, score: 42.000" 1268. .21858
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frame: 1, quality: good, score: 57.000"
/rpt_family="ALU"
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/rpt_family="MER31"
25451
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frame: 0, quality: excellent, score: 79.000"
                                                                                                                                                                                                                                                                                                                                                                                                complement(19351, .19626)
/rpt_family="ALU"
19697, .19833
/rpt_family="ALU"
20425, .20701
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2744. .27765
/rpt_family="ALU"
complement(28025. .28395)
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9017, 1000
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complement(15626...
/rpt_family="ALU"
complement(15950...
/rpt_family="ALU"
16665...17493
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complement(26118.
/rpt_family="ALU"
26645. .27013
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14946. 15122
/rpt_family="L1"
15173. 15445
15584. 15619
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7507
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complement(18269.
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1922. .22503
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19245.
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Query Match
Best Local Similarity
Matches 21; Conserv
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/db_xref="PID:9212260"
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/translation="WTSLLFLVLISVCWAEPHPDNSSLEHERIIHIQEENGPRLLVVA
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/rpt_family="THE1"
complement(28597. .28876)
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complement(29166. .29667)
/rpt_family="MER9"
complement(29979. .30276)
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Deak, F. Kiss, I., Sparks, K.J., Argraves, W.S., Hampikian, G. and Goetinck, P.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Joseph Manner (2007) (1974)

frame: 2, quality: excellent, score: 94.000"

frame: 2, quality: excellent, score: 94.000"

/prLfamily="ALU"

/prLfamily="MERI"

/prlfamily="Merion"

/prlfamily="Merio
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frame: 1, quality: excellent, score: 97.000"
34376. 34477
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Proc. Natl. Acad. Sci. U.S.A. 83, 3766-3770 (1986)
8623315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Chicken cartilage link protein mRNA, complete cds.
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Pred. No. 1.2e+02;
0; Mismatches 3;
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/organism="Gallus gallus"
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136. .1203
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complement(34062. .34170)
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35483. 35637
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Best Local Similarity 87.0%;
Matches 20; Conservative (
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M13212.1 GI:212259
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CHKLNKPA/c
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VERSION
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9212262
M35036.1 G1:212262
cartilage link protein.
2 of 5
Chicken (domesticus, strain White Leghorn) 9-day embryo DNA, clones lambda gLP39.13 and lambda gLP33.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Draft entry and computer-readable sequence for [1] kindly submitted by I.Kiss, 04-JUN-1990.
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Kiss, I., Deak, F., Mestris, S., Delius, H., Soos, J., Dekany, K., Argraves, W.S., Sparks, K.J. and Goetinck, P.
Structure of the chicken link protein gene: Exons correlate with Proc. Natl. Acad. Sci. U.S.A. 84, 6399-6403 (1987)
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-1990
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Neurospora crassa cytoplasmic dynein heavy chain (ro-1) gene,
Complete cds.
L31504
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/note="cartilage link protein mRNA and introns"
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                                                                                                                                                                                                              Query Match 66.7%; Score 18; DB 4; Length 1910; Best Local Similarity 80.8%; Pred. No. 1.6e+02; #ches 21; Conservative 0; Mismatches 5; Indels
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llarity 80.8%; Pred. No. 1.6e+02;
Conservative 0; Mismatches 5; Indels
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/note="cartilage link protein intron
a 90 c 113 g 112 t
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/number=3
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us-09-037-472-1.rge

ORGANISM

KEYWORDS SOURCE

NID VERSION

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE

FEATURES

gene

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LUCHARKEPOATYSTADTGEREAMERYOK NOLMEDFPLDELLSATTLTKVOES IGOT
ILKHARKEPOATYSTADTGEREAMERYOK NOLMEDFPLDELLSATTLTKVOES IGOT
ILKHARKEPOATYSTADTGEREAMERYOK NOLMEDFPLDELLSATTLTKVOES IGOT
SIFRAMDES IRETTNYAREVTERRIKEFIFT INPHEALGSELOKUDYBEFKOYMKOAG
SIFRAMDES IRETTNYAREVTERRIKEFIFT INPHEALGSELOKUVHNERDHHEOLO
RT IINVLGPKATYNGI VTASGANG VAVVEETGDVDAVDEVKOAMEALKDVDLLLCTRE
GTEKWYRAEN IYNERYAPKENSI I JARLBRAARANGLHDLPPVSGAI IWARQI ERQ
LDQYMKKVEQVLGSDWALHTEGGKLONESDERRKKLDTRPFERAMEDVYRKOI SISG
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FRAVSLMESVRTFAQTINRQI SDMSEVAVLLSGGHRNDVYTLISKGI PLRWETFVNTYEVP
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KTREIGAVVOKALNEL
KTREIGAVVOKALNEL
KTREIGAVVOKALNEL
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KRI REIGAVVOKALNEL
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MTANSTAEANRETIT IV VJOSGBALRAKITABENKVNNKI REIRBONDER SVANASL
STIMKNLNELRETIKNSVOPRK TRASIDNLIKMTKEMPSRAROYAREBLIGONVLROLL
KVNSILGELKSBARORHWÄNL KYNOKTROTTENT
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BYYYKEFEERSSKREKLNRYHVLEDIWIDVOROWYLEGVFHGNADIKHLLPIESS
RFONINSEFLAWMKNYGNVLDVLIPNVOKSLERLAELLNKIOKAGESTLEKERV
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VRLKKEINLVKTPRINDWLALLENOWKYTLAELLAEAVDEFTPIFSSENVDRDALIKF
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RKKCEQLITECYHQRDYIEKLYKLNANSWHTWMLLQMRYYNPEGDFLQRLHIKMAN
AKLNGFEYLGVPDRLYPLDTDRCFLTLTLQDLGQRAGYYYNPEGDFLQRLHIKMAN
QLGRFTLVFCCODTFDNQAMGRIFLGICQYQAMGCRDEFNRLEEKILSAVSQQIQDIQ
LGLKWGAEDEKAQIELDGRQIHVNANAGIFITMNFGYAGRSNLPDNLKKLFRSVAMSK
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SEQGPTSSPYEILQIYLHNGLAPYFDASTKSQOLLNGARGRPDVDAKTGIPVTKKRWT
ELELSLSHLQQNVEIPEVSLPFHPLVQSTLEEAATKNVKPSIDLLPATVLADSTFLNN
                                                                               Neurospora crassa
Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
Sordariales; Sordariaceae; Neurospora.
1 (bases 114313)
Plamann,M., Minke,P.F., Tinsley,J.H. and Bruno,K.S.
Cytoplasmic dynein and actin-related protein Arpl are required for normal nuclear distribution in filamentous fungi
J. Cell Biol. 127 (1), 139-149 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOATVNNWIKSIOVITKMTRDPTTGTANQEINFWLSMEAALEGIENQLRSEGVMLTLD
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GLKRARLLETGDAESLGPEDVVEPEIIVQSIRETIAPKLIKSDVEIMMEIESVCFPGV
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VOSOAADLLQEFLTRDNLINEVLKEAANYEHIMEFTVARVLSTLFSLLNKAVRDIIEY
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GTSSLIDFTVTMPQGEWQTWQQHVPTIEVNTHSVTQTDVVIPTLDTIRHEDVLYSWLA
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cytoplasmic dynein heavy chain.
Neurospora crassa DNA.
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GKITELTERHELDEVAQYVKLYNEKREDLEEQORHLNYGLEKLROTYDKVKRELRYTES
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GIVRRDDFIASIVNEFUNEKQMTSLEVKRRNETELANPEFTEKVNRASKACGPLVOWY
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FGNPILLODAEHLDPVLNHYLNKEYQKTGGRVLIOLGKQQIDESPAFKIYLSTRDFSA
                                                                                                                                                                                                                                                                                                                                                                                                    TFAPDICSRTTFVNFTVTQSSLQTQSLNEVLKSERPDVDERRSNLIKLQGEFKVHLRQ
LEKKLLQALNESRGNILDDDHVIETLETLKTEAAEISAKMSNTEGVMAEVEQITLQYN
IIARECSAVFAVLEQLHYLNHFYRFSLQYFLDIFHSVLRGNPHLANETNHNVRRDIIV
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IMDESNVLDSGFLERMNTLLANAEVFGLFEGDDLAALMTACKEGAQRQGLLLDSQEEL
                                                                                                      YKWFTGQIVKNLHVVFTMNPPGEDGLSSKAATSPALENRCVLNWFGDWSDQALFOVAH
ELTHSVDLDRPNWTAPDTIPVAYRGLNLPPSHREAVVNAMVYIHYSLQRFNAKLLKQO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDLFVATFKRTALGLLQKDRITLAMLLAQASPYKMDKGLLDIILDERIEGKDVSIDQN
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EVSHDAEDEQKDAATGGDLVVPSGTSLQEFMGWIQKLPEREPPTYLGLPANAEKLLLV
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EGLIRIWAHEALRLFQDRLVDEEERKWTDDAVRRIAMEYFPTIDEHKALGGPILFSNW
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Homo sapiens Chromosome 12q24 PAC RPCI3-462E2 (Roswell Park Cancer
Institute Human PAC library) complete sequence.
AC003029
AC003029.1 GI:3366554
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Best Local Similarity
Matches 21; Conserv
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ement(80=
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omplement(900)
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lement(427
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/rpt_family="AluJo"
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761. .4893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="FRAM"
507. 7700
                                                                                                                complement(2374. .2612)
/rpt_family="Alusx"
complement(2631. .2799)
/rpt_family="LIMC2"
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complement(7800. .7943)
/rpt_family="Alusg"
                 /rpt_family="MIR"
complement(2001. .2165)
/rpt_family="FRAM"
                                                                                                                                                                                                 complement(2800. 3099)
/rpt_family="Alusc"
complement(3100. 3220)
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/rpt_family="AluJo"
                                                                                                                                                                                                                                                                                                                         complement(3608. .4064)
/rpt_family="L1MB7"
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/rpt_family="Alusg"
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complement(12530. .125:
/rpt_family="AT_rich"
12631. .12765
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.2100. .12229
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rpt_family="AluJb"
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1996. .12094
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1214. .11379
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1381. .11681
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                                            Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Metazoa: Catarrhini; Hominidae; Homo.

I (bases 1 to 13916)

ORS (Loses 1 to 13916)

Muzny,D., Arenson,A.D., Adams,C., Bunac,C., Carvelli,K., Chang,J., Chacko,J., Chen,J., Ding,Y., Dugan,S., Durbin,J., Forcum,J., Ganesh,R., Garcia,C., Goodman,M., Gorrell,J.H., Haywood,M., Hernandez,J., Jackson,L., Jin,S., Kampal,R., Karpathy,S., Kovar,C., Lau,S., Lee,E., Li,Y., Lichkarge,O., Liu,W., Logan,O., Lu,J., Ly,T., Marondel,I., Martinez,C., Verscher,S., Montgomery,K., Oswal,G., Perez,L., Rashid,N.D., Renault,B., Rowland,K., Savage,L., Scherer,S.E., Shen,H., Simon,M., Stovall,R., Timms,K.M., Todd,J., Vo,O., Williamson,A., Worley,K.C., Yu,W., Kucherlapati,R., Direct Submission

**M. Unpublished**
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/note="Overlaps with bases 1-226 in AC002996."
/note="Region: Overlap with AC002996"
/join (88 . .201,843. .945,1380. .1564,6860. .7024,8688. .8845,12641. .12755,18325. .18759)
/gene="Human nucleus-encoded mitochondrial aldehydedehydrogensse(ALDH)gene" us 74620. x031011. x05409"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (17-SEP-1998) Human Genome Sequencing Center, Department
Submitted (17-SEP-1998) Human Genetics, Baylor College of Medicine, One
Daylor Plaza, Houston, TX 77030, USA
On Jul 31, 1998 this Sequence version replaced gi:2909600.
Sequencing is completed to a minimum standard of double strand
coverage with a minimum of 2 clones and 2 reads with no ambiguities
or 2 chemistries with a minimum of 2 clones and 3 reads with no
ambiguities. If the sequence quality does not meet this standard,
it will be indicated in the annotation.
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                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission

Submitted (27-07-1997) Molecular and Human Genetics, Baylor

College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

(bases 1 to 139166)

Morley, K.C.

Direct Submission

Submitted (31-JUL-1998) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

(bases 1 to 139166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (16-SEP-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 139166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence similarities were identified using Powerblast by Jinghui
Zhang.
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530. .696
/rpt_family="AluJb"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RPC13-462E2"
/chromosome="12924"
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                                        Homo sapiens
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Submitted (109-MXY-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquires: humquery(sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Om Mar 22, 1999 this sequence version replaced gi:4376009.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished: dJ856G1 Contig_ID: 01260 acc-AL033381 Length: 151795 bp.

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Urosophila metanogaster (Subclones in tet Irom Pi clone DSU/UZU (DZS98)) DNA.

Everyotta; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera; Pteryota; Meoptera; Endopteryota; Diptera; Brachycera; Pteryota; Meoptera; Endopteryota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.

CE 1 (bases 1 to 51009)

RS Celniker; S. E., George, R. A., Galle, R. F., Hoskins, R. A., Balzej, R. G., Chew, M., Doyle, C. M., Farfan, D. E., Flanagan, J., Houston, K. A., Hummasti, S. R., Karra, K., Kearney, L., Kim, S. H., Lee, B., Lomotan, M. A., Mak, J., Mazda, P., Mok, M.; S. Woshrefi, A. R., Moshrefi, M., Nixon, K., Pacleb, J. M., Park, S., Feiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K. H., Whitelaw, K. R., Yee, A., Zhang, R., Zieran, L. L. and Kimmel, B. George, Drosophila chromosome, region 22E1-22E1

Grayoni, A., Arcaina, T., Baxter, E., Blazej, R. G., Chavez, C., Chew, M., Doyle, C. M., Farfan, D. E., Flanagan, J., Houston, K. A., Appayani, A., Arcaina, T. T., Baxter, E., Blazej, R. G., Chavez, C., Chew, M., Doyle, C. M., Farfan, D. E., Flanagan, J., Houston, K. A., Lomotan, M. A., Max, J., Wazda, P., Mok, M. S., Moshrefi, A., Nixon, K. Pacleb, J. M., Park, S., Pfeiffer, B., Punch, E., Shir, E., Twomey, B., Wan, K. H., Whitelaw, K. R., Yee, A., Zhang, R., Shir, E., Twomey, B., Wan, K. H., Whitelaw, K. R., Yee, A., Zhang, R. Direct Submission

Albritted (07-MAR-1998) Drosophila Genome Center, Lawrence Berkeley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC004340 51050 bp DNA INV 07-JUL-1998
Drosophila melanogaster DNA sequence (Pl DS07020 (D238)), complete
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Pred. No. 1.5e+02;
0; Mismatches 5; Indels
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/db_xref="taxon:9606"
/chromosome="6"
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80.8%;
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Matches 21; Conservative
     Direct Submission
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Homo sapiens chromosome 6 clone 856G1, WORKING DRAFT SEQUENCE, in
/standard_name="DWC10/DWC11"
/note="GDB:179565, Chr. 12q24.2-1-2q24.2, Homo Sapiens"
13248. 13548.
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//rpt_family="AluSx"
complement(17550. .17928)
/rpt_family="L2"
/rpt_family="AluJo"
/rpt_family="AluJo"
18311. .18642
/gene="Human nucleus-encoded mitochondrial aldehyde
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 151795)
Phillips,S.
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1987. 20151
/rpt_family="Alusp"
complement(20254. 205551)
                                                                                                                                                                                                                                                                                                                                                                                                                             complement(16333. .16541)
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complement(16658. .16956)
/rpt_famlly="Alusx"
16992. .17186
17205. .17186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Alusx"
complement(20559, 210f)
/rpt form
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                                                                                                                                                           /rpt_family="AluJo"
complement(14148. .14404)
/rpt_family="AluJb"
                                                                   /rpt_family="Alusx"
complement(13595. .13622)
/rpt_family="AT_rich"
13999. .14103
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18807. .19105
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complement(19388. .1
                                                                                                                                                                                                                                                                                                                           5472, .15/bo
/rpt_family="Alusx"
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ULOSOPHINA MELABORASTEL

EUKATYOTA; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Bacchycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 85139)

ORS Celniker; S.E., George, R.A., Galle, R.F., Hoskins, R.A.,
Svirskas, R.R., Harris, N.L., Adpayani, A., Arcaina, T.T., Baxter, E.,
Flanagan, J., Huutston, K.A., Hummasti, S.R., Karrak, Kearney, L.,
Kim, S.H., Lee, B., Lomotan, M.A., Maxda, P., Mok, M.S.,
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, R.R.,
Yee, A., Zhang, R., Zieran, L.L. and Kimmel, B.
Sequencing of Alcohol dehydrogenase region

Unpublished (1997)

ORS Martin, C.H., Arcaina, T.T., Bondoc, M.M., Chiang, A., Critz, P.A.,
Davis, C.A., Doyle, C.M., Ericsson, C.L., Farfan, D.E., Gunning, K.M.,
K.A., Jaklevic, M.A., Kadner, K.E., Kim, S.F.,
Ko, C.L., Lewis, K.D., Lim,, Lindquist, K.J., Lomotan, M.A.,
Luste, V.M., Machrus, M.U., Mayeda, C.R., Miquel, T.M., Miller, C.A.,
Mok, M.S., Pacleb, J.M., Patel, S.G., Santos, R.F., Subramanian, S.,
Wan, K.H., Whitelaw, K.R., Yee, A., Yeh, R.T., Yu, C. and Palazzolo, M.J.
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Jul 7, 1998 this sequence version replaced gi:3228456.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send email to drosophila@mingc.lbl.gov.
Library location: 12-74.
Library 
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L81427 L36203 L81426 L39670 L39668 L36294 L36285 L36295 L39667
L36296 L36297 L36299 L36291 L36297 L36284 L39671 L39665 L39669
L36292 L36293 L36302 L36290
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Submitted (22-APR-1997)
On Aug 20, 1997 this sequence version replaced gi:1945585.
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21; Conservative 0; Mismatches 5; Indels
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/chromosome="2L"
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Berkeley Drosophila Genome Project
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Lawrence Berkeley National Laboratory, MS 64-121

Berkeley, CA 94720

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive who site (http://fruitiy.berkeley.edu/sequence/) or send email to drosophila@mipc.lbl.gov.

Library location: 58-72.

Library location: 58-72.

Library location: 58-72.

Corganism="Drosophila melanogaster"

Adb_xrain="Drosophila melanogaster"

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us-09-037-472-1.rng

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

(without alignments) 31.709 Million cell updates/sec September 18, 1999, 04:59:15; Search time 213.04 Seconds Run on:

US-09-037-472-1 27 Perfect score:

1 AAGCTIGITCIACCACCIGAACTAGGC Sequence:

IDENTITY\_NUC Scoring table: 311585 seqs, 125096042 residues Searched:

N\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description
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D	ı m	T70316	X02988	x16611	V78683	V75647	T92382	V77989	N40312	x20576	X13096	026727	V79270	V78290	V78258	V78053	V78055	V78042	V78001	V77971	V77942	V77932	V77850	V77853	V77425	V78877	V78855	V78854	V78664	V78574	V78545	33	34	38	036747	8	~	4	0724	3485	844	80605	024
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Length		22	5701	21	327	633	687	648	1253	6422	8160	7753	59	400	361	400	400	401	553	400	400	475	1171	400	6591	237	239	239	411	339	400	381	400	1421	1393	2259	384	1557	1557	4190	1922	٦,	110000
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Score	27	22	22	21	٦,	17.4	٠.	۲.	17	_		٠ م	٠	٠,	٠,	٠,	٠,	٠.	٠,	٠,	٠,	٠,	٠,	٠ ،	٠.	16.6	٠,	٠,	٠,	٠,	٠,	٠,	٠,	٠.	٠,	•	16.2	٠	•		16.2	٠	
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Primer for detecting genetic predisposition to periodontal disease.

Periodontal disease; gingivitis; periodontitis; polymorphism; interleukin-1 alpha; IL-1A; interleukin-1 beta; IL-1B; primer; PCR; Synthetic.

Synthetic.

W09706180-A1.

T70316 standard; DNA; 22 BP.

19-OCT-1997 (first entry)

T70316;

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RESULT T70316

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The first is the and in large. Use all the called the citizen properties occur controlled to the controlled the controlled to controlled to the controlled to controlled to controlled to controlled to the controlled to contro
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        Polynucleotide seq
Borrelia burgdorfe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RICH/) RICHARDSON R.

Duff G, Rennie I, Richardson R;

WPI: 98-240835/21.

Predicting increased risk of sight-threatening diabetic retinopathy
comprises identifying genetic polymorphism pattern for genes
IL-1A, IL-1B and IL-1RN, useful to allow treatment before clinical
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Interleukin-1-alpha primer 1 (-967/-945).
IL-1-alpha; genetic polymorphism; PCR; primer; amplification;
IL-1-alpha; genetic polymorphism; PCR; primer; amplification;
sight threatening diabetic retinopathy; interleukin-1-alpha;
interleukin-1-beta; interleukin-1RN; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 27;
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100.0%; Score 27; DB 1; 1
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                            ALIGNMENTS
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X30293
                                                                                                                                                                                                                                       V32389 standard; DNA; 27 BP.
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73
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10-OCT-1996; GB-021129.
(DUFF/) DUFF G.
60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
W09815653-A1.
16-APR-1998.
16.2
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Pred. No. 0.25;

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Best Local Similarity 100.
Matches 22; Conservative
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X16611
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New isolated nucleic acid encoding the new human cytokine Tango-77 - used to inhibit inflammation and to screen for specific modulators

Example 5; Figure 3: 226pp; English.

X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

CX02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

CX02056-X03048 and X22301-X22304 are overlapping BAC genomic sequences

CX03057-X0304-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X0301-X
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Human IL-1ra BAC contiguous DNA sequence 33.
Tango-77: human: IL-1ra: cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; requiation; asthma: rheumatori arthritis; chronic myelogenous leukaemla; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                                Transcriptor of patient's genetic polymorphism pattern - allows reduction of increased periodontal disease severity claim 3: Page 25; 33pp; English.

Claim 3: Page 25; 33pp; English.

Claim 3: Page 25; 33pp; English.

Cor identifying a genetic predisposition to periodontal disease by detecting the presence of DNA polymorphisms in the gene sequences for interleukin-1 alpha (IL-1A) and interleukin-1 beta (IL-1B).

Alleles associated with severe disease were identified as IL-1B, alleles a sociated with severe disease were identified as IL-1B, alleles 2 together with IL-1B (Tag1) allele 2. The primers are used to amplify DNA from a blood or tissue sample and products are subjected to restriction digestion to determine the polymorphism pattern. A single base variation (C/T) polymorphism at IL-1A base -889 can be identified using primers (T70316 and respectively. An Nocl site is created if C is available at -889, but not if T is present.

Sequence 22 BP; 5 A; 7 C; 4 G; 6 T;
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0.12;
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Pred. No.
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02-JUL-1998; US-091650.

04-AUG-1997; US-054646.

(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

Pan Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.5%; Scor.
100.0%; Pre
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quence 5701 BP; 1729 A;
                                       (KORN/) KORNMAN K S.
(MEDI-) MEDICAL SCI SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 TGTTCTACCACCTGAACTAGGC 27
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Best Local Similarity 100.
Matches 22; Conservative
02-AUG-1996; U12455.
03-AUG-1995; US-510696.
                                                                                 Kornman KS;
                                                                               Duff GW, Kornman F
WPI; 97-154207/14.
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WO9906426-A1.
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X02988
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DB 1; Length 5701;

81.5%; Score 22;

Query Match

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Mew method of determining a patient's susceptibility to inflammatory disorders - by detecting the presence of an IL-1 (4411232)

The protection of designing treatment strategies that modulate the activity of proteins produced by the IL-1 gene cluster

The activity of proteins produced by the IL-1 gene cluster

Claim 3: Page 33: 49pp; English.

C A method has been developed for determining a patient's susceptibility to an inflammatory disorder. The method comprises the detection of an interference its presence indicates susceptibility to an inflammatory disorder. Al667 to X16631 represent PCR primer used in the method for detecting the IL-1 (44112332) haplotype. The method provides kits for detecting the IL-1 (44112332) haplotype. The method provides kits for the early prediction of a patient's susceptibility to an inflammatory corpusty artery disease, osteoporosis, nephropathy alsorders, including coronary artery disease, osteoporosis, nephropathy in diabetes mellitus, alopecia areata, Graves disease, systemic lupus cervithmancous. Inchem sclerosis and utcerative colitis. The detection of alsorders, including diabetic retinopathy, juvenile chronic arthritis, alopecia areata disease, osteoporosis, nephropathy coronarising diabetic retinopathy, juvenile chronic arthritis, protections of disease-associated haplotype enables determination of which alleles are constrained the activity of proteins produced by the IL-1 gene cluster. Some alleles from the IL-1 gene cluster are associated with particular inflammatory diseases, and insufficient IL-1 production appears to act centrally in the pathology of these diseases. Therefore, the use of IL-1 gene clusters is useful in determining genetic susceptibility to act gene clusters is useful in determining genetic susceptibility to act conformatory diseases, including those with a multifactorial etiology with a polygenic component.
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                                                                                                                                                                                                                                                                                                                                                                                             29-APR-1999 (first entry)
Interleukin I (44112332) haplotype PCR primer #5.
Interleukin 1; IL-1; haplotype; inflammatory disorder; alopecia areata; Coronary artery disease; osteoporosis; nephropathy; diabetes mellitus; Graves disease; systemic lupus erythamatosus; lichen sclerosis; ulcerative colitis; PCR primer; ss.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mismatches
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100.08; Pr
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100.0%; Pre
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Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-DEC-1998, C01481.
21-MAY-1997; GD1481.
29-MAY-1997; GB-011040.
(CAMP/) CAMP N J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Camp NJ, Cox A, De WPI; 99-080814/07.
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W09854359-A1.
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                                                                                                                                                                                                                                                                                                                                                                                          29-APR-1999
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V78683
ID V7
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18-MAR-1996; 060732,
18-MAR-1996; JP-0607
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V77989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents one of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for including cellulities.
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                                                                                                                                                                                                                                                                                                                                                                                          Polynicleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines.
Claim 1, Page 2938, 3271pp; English.
This sequence represents one of 5191 Staphylococcus aureus DNA sequences
                    16-MAR-1999 (first entry)
Staphylococcus aureus contig SEO ID #4372.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
Etaphylococcus aureus.
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Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
Staphylococcus aureus.
EP-786519-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
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in the production of
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07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash_SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 18; DB
80.8%; Pred. No. 12;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-S.aureus vaccines
Claim 1; Page 1924; 3271pp; English.
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07-JAN-1997; 100117.
05-JAN-1996; US-009861.
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Best Local Similarity
Watches 21; Conserv
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WPI; 97-37
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V75647/
qq
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating computer readable medium.
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Claim 7: Page 11-12: 16pp; Japanese.

The present sequence encodes nitrile hydratase subunit beta, a novel protein isolated from Bacillus smithii. The protein has hydration activity for converting acrylonitrile into acryloamide. It is useful for producing amide from nitrile by biological catalysis.

Sequence 687 BP; 212 A; 112 C; 173 G; 190 T;
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Bacillus smithii nitrile hydratase subunit beta encoding DNA.
'itrile hydratase subunit alpha; nitrile hydratase subunit beta;
acrylonitrile; acryloamide; biological catalysis; amide;
thermally stable protein; ds.
Bacillus smithii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 T;
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/product= Nitrile_hydratase_subunit_beta
/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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P-PSDB: W32621.
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T92382/c
TD T92382 standard; DNA; 687 BP.
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86.4%;
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Best Local Similarity 94.7
Matches 18; Conservative
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Best Local Similarity 86.4
Matches 19; Conservative
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Gaps

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V77989

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NWIT; 99-081273/07.

New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis (Z1aim 1: Page 593-597; 1150pp; English.

X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detection diseases related to Borrella infections in animals, and for the production of biosynthetic products such as enzymes.

Sequence 6422 BP; 1614 A; 1888 C; 1547 G; 1361 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1999 (first entry)
Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
Treponema pallidum.
                                                                                                                                                                                   Prodn. of interferon in yeast - by use of recombinant DNA segment contg. suc 2 promoter linked to interferon gene Example: Page 48: 53pp; English.

The inventors claim a managed for the prodn. of interferon in yeast by use of recombinant DNA segment contg. suc 2 promoter linked to interferon gene. The interferon synthesis can be regulated over a broad rangee by changes in the culture medium, e.g. synthesis is depleted. Also claimed is yeast strain ATCC 20644-CGY144.

Sequence 1253 BP: 373 A; 268 C; 244 G; 368 T;
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Deficience faccalis genome contig SEQ ID NO:159.

Enterococus faccalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.

Enterococcus faccalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.0%; Score 17; DB 1; Length 1253; 80.0%; Pred. No. 42;
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                                                 Fink GR, Knowlton
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Pred. No. 53;
0; Mismatches
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                                          Botstein D, Bowden DW, Davis RW, 1
Mao J, Taunton-Rigby A, Vovis GF;
WPI; 84-088509/14.
P-PSDB; P40741.
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           (COLB ) COLLABORATIVE RES INC.
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80.0%;
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23-JUN-1998; U13041.
24-JUN-1997; US-050667.
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Best Local Similarity
Matches 20; Conserv
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Matches 2
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X20576
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Claim 1: Page 2639-2640; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM) or DO-RAM. Homology searches using that sureus DNA sequences allows putative functions to be assigned to that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a Nit for the immunodetection of the polypeptides can also be used in a Nit for the immunodetection of the contract of
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                                                                                                                                                                                                                                                                                                                                                               /*tag= a // the se bases represent a line of missing text in /note= "these bases represent in the specification. They the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
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                                                                                                   Staphylococcus aureus contig SEQ ID #3678.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-3405-1992 (first entry)
Sequence of human leukocyte interferon (leIFN) gene.
Interferon; yeast expression vector; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 C;
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 TIGITCIACCACCIGAACTAGGC 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.78;
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                                                                            (first entry)
V77989 standard; DNA; 648
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Matches 19; Conservative
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07-JAN-1997; 100117.
05-JAN-1996; US-009861.
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US-418521.
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                                                                                                                                                                                                                                                                                              Staphylococcus aureus.
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09-SEP-1983; U
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                                                                        16-MAR-1999
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RESULT 13
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 898-902; 2084pp; English.
A computer readable medium has been developed which has recorded on it
A computer readable medium has been developed which has recorded on it
12982 nucleotide sequences isolated from the Enterococcus faecalis genome.
12038 to Mi3919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                  04-MAY-1998; U08985.
14-NOY-1997; US-044019.
06-MAY-1997; US-044011.
16-MAY-1997; US-044011.
16-MAY-1997; US-044011.
16-MAY-1997; US-044011.
16-MAY-1997; US-044011.
16-MAY-1997; US-044011.
18-MAY-1997; US-044011.
18-MAY-1997; US-04011.
18-MAY-1997; US-04011.
18-MAY-1997; US-04011.
18-MAY-1998; US-04011.
18-MAY-1997; US-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Encodes exons XV to XVIII of human hepatocyte growth factor.
HGF: enhance growth; preparing transgenic animals; hepatic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2292 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                 use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 8160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1654 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.2%; Score 16.8; I 90.0%; Pred. No. 68; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1463 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/note= "exon XVIII"
7492. .7497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clinical diagnostic reagent; drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101. .241
/*tag= a
/note= "exon XV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3366 TGTTCTAGCTCCTGAACTAG 3385
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/*tag= //nof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-1992.
19-NOV-1990; 314548.
19-NOV-1990; JP-314548.
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(TOYM ) TOYOBO KK.
WPI; 92-265591/32.
P-PSDB; R25692.
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Polynucleotide(s) and proteins derived from Staphylococcus aureus - stored on computer readable medium and used in the production of a natis: Aureus vaccines

Tain 1: Page 3132; 3271pp; English.

Claim 1: Page 3132; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences

CC the invention. The DNA sequences are recorded on a computer readable

medium, preferably selected from a floppy or hard disk, random access

CC medium, preferably selected from a floppy or hard disk, random access

CC that protein-enroding or requilatory ROWI or CD-ROW. Homology searches using

CC that protein-enroding or requilatory regions of commercial, therapeutic or

CC that protein-enroding or requilatory regions of commercial, therapeutic or

CC that protein-enroding or requilatory regions of commercial, therapeutic or

CC that protein-enroding or requilatory regions of commercial, therapeutic or

CC that protein-enroding or requilatory regions of commercial, therapeutic or

CC that protein-enroding or requilatory regions for identified and these polypeptides can

CC industrial importance can be obtained sequences to storemyellitis,

CC Saureus in a vaccine composition against S. aureus infection of

CS. Saureus in a sample. S. aureus is implicated in numerous human diseases.

CC skin and surgical wound infections, food poisoning, osteomyellitis,

CC syndrome, etc. Organisms transformed with the DNA sequences can be used

CC (and their fragments) are useful as primers or probes for isolating

CC (and their fragments) are useful as primers or probes for isolating

CC committer readable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus contig SEQ ID #4959.
Computer readable medium: vaccine: S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome:
                                                                                                                                                                                                                                                                                                                                             Gaps
useful for diagnosis and transgenic animal prepu.

Liansgenic animal prepu.

Disclosure; Page 22; 28pp; Japanese.

This sequence contains exons XV to XVIII of human hepatocyte growth factor. See also R25676-92, 026713-27.

Sequence 7753 BP; 2567 A; 1177 C; 1243 G; 2766 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                         Length 7753;
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                                                                                                                                                                                                                                                                                                                                          4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SC1 INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                         Score 16.6; DE
Pred. No. 84;
0; Mismatches
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); Mismatches
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82.6%; Pred. No. 43;
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82.6%;
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ID V78290 standard; DNA; 400 BP.
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                                                                                                                                                                                                                                                                      Query Match 61.5
Best Local Similarity 82.6
Matches 19; Conservative
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Sequence 59 BP: 16 7
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07-JAN-1997; 100117.
05-JAN-1996; US-009861.
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EP-786519-A2.
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nes 19; Conserv
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Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences

Claim 1; Page 2772-2773; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences

Cf the invention. The DNA sequences are recorded on a computer readable

medium, preferably selected from a floppy or hard disk, random access

medium, preferably selected from a floppy or hard disk, random access

medium, preferably selected from a floppy or hard disk, random access

medium, preferably selected from a floppy or hard disk, random access

the S.aureus DNA sequences allows puttive functions to be assigned so

that protein-encoding or regulatory regions of commercial, therapeutic or

industrial importance can be obtained. Specifically, sequences which are

likely to encode antigens have been identified and these polypeptides can

be used in a vaccine composition against S.aureus infection. The

polypeptides can also be used in a kit for the immunodetection of

S.aureus in a sample. S.aureus is implicated in numerous human diseases,

including cellulitis, eyelid infections, food poisoning, osteomyelitis,

syndrome, etc. Organisms transformed with the DNA sequences can be used

for recombinant production of the polypeptides. The new DNA sequences

content readable medium.
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                                                                                                                                                                                                                    /note="these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specificatio. for this DNA sequence"
                                 Staphylococcus aureus contig SEQ ID #3979.

Computer readable medium; vaccine; 5.11reus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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Computer readable medium; vaccine; S.aureus infection; immunodetection;
Computer readable medium; vaccine; S.aureus infection; infection;
cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
skin infection; surgical wound infection; scalded skin syndrome;
toxic shock syndrome; ds.
Staphylococcus aureus.
EP-786519-A2.
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Pred. No. 56;
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                                                                                                                                                          Location/Qualifiers
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O7-JAN-1997.
O5-JAN-1996: US-009861.
(HUMA-) HUMAN GENOME SCI INC.
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82.6%;
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07-3AN-1997.
05-3AN-1996: US-009861.
(HUMA-) HUMAN GENOME SCI INC.
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                16-MAR-1999 (first entry)
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                                                                                                                                              Staphylococcus aureus.
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Best Local Similarity
Matches 19; Conservat
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of this sequence represents one of 5191 Staphylococcus aureus DNA sequences of the Invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access compared from a floppy or hard disk, random access compared from a floppy or hard disk, random access compared from a floppy or hard disk, random access compared from a floppy or hard disk, random access compared from a flop protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition adainst S aureus infection. The polypeptides can also be used in a kit for the immunodetection of saureus in a sample. S aureus is fimplicated in numerous human diseases, including cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences core contained on the constant of the saureus DNA sequences contained on the
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                                                                 Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-S.aureus vaccines
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Job time: 1678 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 C;
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82.6%;
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Sequence 361 BP; 104
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Best Local Similarity
Matches 19; Conserv
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us-09-037-472-1.rst

Sequence:

Run on:

Searched: Database

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RESULT 1
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LOCUS
DEFINITION
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VERSION
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                                                                                                                                     (without alignments)
37.906 Million cell updates/sec
                                                                                                                 September 18, 1999, 05:46:43; Search time 1405 Seconds
                    Compugen Ltd
GenCore version 4.5
Copyright (c) 1993 - 1998 Comp
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                                                                            nucleic search, using sw model
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em_est2: *
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em_est6: *
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em_est10: *
em_est11: *

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gb_est32:*
em_est20:*
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AA607268 vm92h05.r

AA61861 vr44a05.s

AA422881 EST3551

AA422885 vd47c06.s

AA824084 vr66c03.s

AII61663 A004P75U

T05736 EST03625 Fe

F13213 HSC3KC111 n

T66000 yp91q05.r1

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AA004527 zh91a09.r

AA004527 zh91a09.r

AA004527 zh91a09.r

AA004527 zh91a09.r

AA004528 EST32100 HU

T35252 EST3210 HU

T35251 EST31965 HU

T35551 EST81965 HU

T35551 EST81969 HU

R17871 yg7086.r1

R18749 yg17c08.r1

R18749 yg17c08.r1

R18749 yg17c08.r1

R18749 yg17c08.r1

R3551 EST177333

AA300763 EST177333

AA300495 EST178919

AA300495 EST178410

AA311686 EST182410

AA31686 EST182410

AA316869 EST182410

AA316869 EST88240

AA316869 EST88240

AA3168029 EST188211

AA806156 AK47009.s

A15582929 fD78002.y

A15582929 fD78002.y

A1558220 LS142A R
                                                                              N88530 K3598F Huma
                              Pred. No. is the number of results predicted by chance \,^{\circ}0 have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                      Description
                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                    SUMMARIES
                                                                                   AA607268
AA581861
AA322885
AA824084
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TO5736
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AA306551
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AA310973
AA311686
AA314612
AA316439
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55:
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K3598F Human fetal heart, Lambda ZAP Express Homo sapiens CDNA CLONE K3598 5', mRNA sequence.

91441732
N88530.1 GI:1441772

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    459
    /organism="Mus musculus"

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Matches 21; Conserv
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JOURNAL
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                                                                                                                                             FEATURES
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/Organism="Homo sapiens"
/Ob_xref="taxon:9606"
/Clone="K3598"
/Clone=lib="Human fetal heart, Lambda ZAP Express"
/Clone=lib="Human fetal heart, Lambda ZAP Express"
/Lab_host="E. coli XLI-Blue"
/Lab_host="E. coli XLI-Blue"
/Lab_host="Test coli XLI-Blue
/Lab_host="Test coli XLI-
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Mooris,M., Tan,E., Underwood,K., Moore,B., Theisling,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 405)
                                                                                                                                                                                                                                                                         Contact: Liew CC

Department of Laboratory Medicine and Path biology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5GlL5
Tel: 4169788758
Fax: 4169785650
Email: liewcc@utcc.utoronto.ca
Seq primer: GAAATTAAACCTCACTAAAAGGG.
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On Sep 12, 1996 this sequence version replaced gi:1288177
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 405;
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                                                                                                                                                                                       Unpublished (1996)
On Sep 1, 1995 this sequence version replaced
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The WashU-HHMI Mouse EST Project
                                                                                                                                                   CDNAs from fetal heart (1996)
Unpublished (1996)
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1. .405
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AA607268.1 GI:2456161
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   Homo sapiens
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                      Liew, C.C.
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ORGANISM
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TITLE
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AA607268/c
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AUTHORS
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KEYWORDS
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/note-Torgan: embryo; Vector: pSPORT; Site_1: Not1; Site_2: Sal1: Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: Sal1(dT): 5'-CGGTCGACCGTTTTTTTTTTTTTTT" CDNAS were cloned into the Not1/Sal1 sites of a pSPORT vector (Life Technologies). Two different size selections: Bl (larger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 459)
Marra M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU-HHMI Mouse ETP Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4442 Ed. 1800
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
Fhis clone is available royalty-free through LLNL; contact the
MGI:612808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA681861 459 bp mRNA EST 05-DEC-1997 vr44a05.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:1123472 5', mRNA sequence.
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1392950.
                                                                                                                                                                                  /organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone=!IMAGE:1005753"
/clone=lib="Knowles Solter mouse blastocyst B1"
/fissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.9%; Score 18.6; Dilarity 84.0%; Pred. No. 55; Conservative 0; Mismatches
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                                                                  MGI:569969
High quality sequence stop: 472.
Location/Qualifiers
1. 525
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inserts) and B3."
129 c 111 g
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Location/Qualifiers
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us-09-037-472-1.rst

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BASE COUNT
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JOURNAL
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AA422885
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SOURCE
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/de_tstage="2-cell"
/lab_host="DH10B"
/note="0rgan: embryo; Vector: pBluescribe (modified);
/note="1">Interview (modified)
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Other_ESTs: THC170844
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68.9%; Score 18.6; DB 37; Length 459;
Best Local Similarity 84.0%; Pred. No. 54;
Matches 21; Conservative 0; Mismatches 4; Indels 0;
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                       /clone_lib="Knowles Solter mouse 2 cell"
                             /db_xref="taxon:10090"
/clone="IMAGE:1123472"
/strain="B6D2 F1/J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 AAGCTTGTTGTCCCACCTCACCTAG 143
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AA331881.1 GI:1984123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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KEYWORDS
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Mus musculus
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 564)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                   1...24
/organism="Homo sapiens"
/db_xref="ArCc (inhost):133506"
/db_xref="taxon:9606"
/clone_lib="Embryo, 8 week I"
/dev_stage="embryo, 8 wks"
/note="Organ: Embryo, 8 weeks; Vector: pBluescript SK-; Site_l: EcoRI; Site_2: XhoI"
a 60 c 60 g 56 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: embryo; Vector: pBluescribe (modified);
Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashUrHMI Mouse EST Project
WashUrHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
Fins clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA422885 564 bp mRNA EST 16-OCT-1997 vd47c06.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:803722 5' similar to gb:X64550 M.musculus mRNA for hyaluronan-mediated motility (MOUSE);, mRNA sequence.
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
On May 8, 1995 this sequence version replaced gi:800408.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
66.7%; Score 18; DB 32; Length 224;
Best Local Similarity 77.8%; Pred. No. 88;
Matches 21; Conservative 0; Mismatches 6; Indels
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/clone="lib="Knowles Solter mouse 2 cell"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH108"
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
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High quality sequence stop: 441.
Location/Qualifiers
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/strain="B6D2 F1/J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 AAGCTCGTTCTTCCACATGCAGNAGC 123
                                                                 Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 423)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                             ö
mRNA prepared from 13,500 2-cell stage embryos. Primer: SalI(dT): 5'-CGGTCGACCGTTTTTTTTTTTTTTTTTTT" . CDNAs were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:614940
                                                                                                                                                                                                                                                                                                                                            AA824084 422 bp mRNA EST 17-FEB-1998 vr66c03.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:1125604 5' similar to 9b:X64550 M.musculus mRNA for hyaluronan-mediated motility (MOUSE);, mRNA sequence.
AA844084
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU'HHM Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1404594.
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                                                                                                                                                      66.7%; Score 18; DB 33; Length 564; ilarity 80.8%; Pred. No. 1.1e+02; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 422.
Location/Qualifiers
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house mouse.
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Matches 21; Conserv
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Sterky,F., Regan,S., Karlsson,J., Hertzberg,M., Rohde,A., Holmberg,A., Amini,B., Bhalerao,R., Larsson,M., Villarroel,R., Van Montagu,M., Sandberg,G., Olsson,O., Teeri,T.T., Boerjan,W., Gene discovery in the wood-forming tissues of poplar: Analysis of Front, Mail. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK; Site_1: SalI; Site_2: NotI; Cambial region tissues, including developing xylem, the meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. CDNA was prepared and cloned into lambda gt22a. DNA was isolated and subcloned into pBluescript SK using SalI and NotI restinon enzymes." 5 others
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                                                                                                                                                                                                                                                                        Al161663 465 bp mRNA EST 03-DEC-1998 A004275U Hybrid aspen plasmid library Populus tremula x Populus tremuloides cDNA 5', mRNA sequence.
                                                           Gaps
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/db_xref="taxon:47664"
/clone_lib="Hybrid aspen plasmid library"
/tissue_type="Cambial region"
/dev_stage="1.5 m actively growing tree"
/lab_host="E.coli"
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       Length 422;
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Department of Biotechnology
Royal Institute of Technology (KTH)
Teknikringen 34, S-100 44 STOCKHOLM, Sweden
Tel: +46 8 790 8287
Fax: +46 8 24 54 52
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       Score 18; DB 39;
Pred. No. 1e+02;
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                                                   0; Mismatches
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Seg primer: CGTTGTAAAACGACGGCCAG
High quality sequence stop: 465.
Location/Qualifiers
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                                                                                                                              2 AGCTIGITCIACCACCIGAACTAGGC 27
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     66.7%;
80.8%;
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C. Ty Match
Eact Local Similarity 80.8
Watches 21; Conservative
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Best Local Similarity 90.5
Matches 19; Conservative
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Best Local Similarity 74.1
Matches 20; Conservative
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                                                           T05736 30-JUN-1993 EST 30-JUN-1993 EST03625 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDF63 similar to Retrovirus-related pol polyprotein, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Fetal brain, Stratagene (cat#936206)"
/note="Vector: LambdaZAP-II; 17-18 wk gestation, female;
oligo-dT + random primed cDNA synthesis; lambdaZAP-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 308)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Corenzo,F., Mitchell,H., Mariage Samson,R., Pietu,G., Pouliot,Y., Sebastiani Kabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome and its expression
                                                                                                                                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; domo.
1 (bases 1 to 337)
Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.
3,400 expressed sequence tags identify diversity of transcripts from human brain
Nature Genet. 4, 256-267 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infant brain cDNA Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                       Other_ESTS: EST03626
Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tex: 3018659056
Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
//db_xref="ArC (inhost):82427"
/db_xref="taxon:9606"
/clone="HFBDF63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13-21.
Location/Qualifiers
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g316886
TO5736.1 GI:316886
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HSC3KC111 normalized
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F13213.1 GI:709258
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Best Local Similarity 80.0
Matches 20; Conservative
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F13213/c
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/tissue_type="total brain"
/dev_stage="3 months old"
/dev_stage="3 months old"
/dev_stage="3 months old"
/dev_stage="3 months old"
/dev_stage="1" is a months old;
/dev_stage="3 months old;
/dev_stage="3 months old;
/dev_stage="3 months old;
/dev_stage="3 months old;
/dev_stage="1" is a months old;
/dev_stage="1" is a
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 526)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Hillier,L., Lennon,G., Becker,M., Edoy,M., Cap.M., Le,M., Levande,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevarkis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
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Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generores_library_idt: C; Genexpress_sequence_idt: ylc-3kcll
Insert Length: 1240 Std Error: 0.00
Seq primer: (-21)M13_universal
High quality sequence stop: 298.
Location/Qualiflers
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                                                                                                                                                         Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de 1/internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Fax: 331619 genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-3kc11"
/clone=lib="normalized infant brain cDNA"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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74.1%; Pred. No. 1.4e+02;
ive 0; Mismatches 7;
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Washington University School of Medicine
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Contact: Wilson RK
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les 20; Conserv
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DEFINITION
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AA004527/c
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Matches
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                                                                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENKATYOCA: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; EUKATYOCA; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 425)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Homissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hulman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rikin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Travaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                      High qality sequence stops: 283 Source: IMAGE Consortium, LLNL The colone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1027 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 283.

Location/Qualifiers

1. 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
   Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB:498329"
/db_xref="taxon:9606"
/clone="IMAGE:78584"
/clone=lib="Stratagene liver (#937224)"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.2%; Score 17.6; DB 21; 83.3%; Pred. No. 1.6e+02;
Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                   Email: est@watson.wustl.edu
Insert Size: 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 AAGGITGITCIACACCCIAAACIA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
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Best Local Similarity
Matches 20; Conserv
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JOURNAL
MEDLINE
COMMENT
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KEYWORDS
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double-stranded cDNA was ligated to Ecc RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified PT7T3 v-ctor. Library went through one round of normalization Library constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA004527 480 bp mRNA EST 07-MAY-1997 zh91a09.rl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens CDNA clone IMAGE:428632 5' similar to contains Alu repetitive element;contains element MER22 repetitive element;; mRNA sequence.
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[Dases 1 to 480)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,M., Le,M., Le,M., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Forballenberg,K., Soares,M.B., Tan,F., Thierry,Mey,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 673 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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97044478
                                                                                                                                                                                                                                                                       /clone="IMAGE:428363"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 425;
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Pred. No. 1.5e+02;
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444 Forest Park Parkway, Box 8501, St. L
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                        /organism-"Homo sapiens"
/db_xref-"GDB:1328132"
/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 AAGCCTCTTCTACCACCTGATCAA 60
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us-09-037-472-1.rst

FEATURES

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/note="Organ: Kidney; Vector: p1713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive Hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDs 132376-1323911, 1456007-1456775, and Patima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV046966 226 bp mRNA EST 18-MAY-1999
AV046966 Mus musculus adult C57BL/6J testis Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tal: 81-298-36-9145
Fax: 81-298-36-9145
Fax: 81-298-36-9196
Fax: 81-298-36-9199
Fax: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 226)

Carninci, P., Shibata, R., Ozawa, Y., Konno, H., Ito, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nilisuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shiqemoto, Y., Shiraki, T., Soqabe, Y., Tomana, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tokota, T., Yoshino, M., Matamabe, S., Yagame, M., Yamamura, T., Yokota, T., RIKEN, Mouse ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
On Jur 22, 1998 this sequence version replaced gi:3247120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.2%; Score 17.6; DB 48; Length 593; 83.3%; Pred. No. 1.7e+02; .ive 0; Mismatches 4; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 t
                                                                                                                                                                                                                                                                                       /clone="IMAGE:2172055"
/clone_lib="NCI_CGAP_Kidll"
/lab_host="DH108"
                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="16"
             Seq primer: -40UP from Gibco
High quality sequence stop: 459
POLYA-No.
                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
Matches 20; Conserv
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AV046966
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.AG.E., Consortium/LLNL at:
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IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 688 Std Error: 0.00 Seq primer: mob.REGA+Er High quality sequence stop: 378.
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Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3137546.
                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
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Pred. No. 1.6e+02;
0; Mismatches 4; Indels 0;
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83.3%; Pred. No. 1...
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/organism="Homo sapiens"
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Best Local Similarity 83.3%
Matches 20, Conservative
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DEFINITION RESULT 13 AI566060

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL COMMENT

BASE COUNT ORIGIN

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399 bp mRNA EST 07-JUN-1994
seq1305 b4HB3MA COt8-HAP-Ft Homo sapiens cDNA clone
b4HB3MA-COT8-HAP-Ft213 5' similar to similar to Mouse MER5 protein,
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Department of Psychiatry,722 W 168th Street, Unit #41, New York,NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 399)

Soares,M.B., Bonaldo,M.F., Jelenc,P., Su,L., Lawton,L and Efstratiadis,A.

Construction and characterization of a normalized cDNA library 95023884
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/dev_stage="testis"
18 g 75 t
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Pred. No. 1.4e+02;
0; Mismatches 4;
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Fax: 2127813577
Email: cuc@cuccfa.ccc.columbia.edu
sense, Ampicillin
Seq primer: M13 Reverse.
Location/Qualifiers
                               Location/Qualifiers
1. 226
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T10245.1 GI:471594
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Best Local Similarity 83.33
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